

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2004, 06:36:22 ; Search time 140 seconds
(without alignments)

6342.296 Million cell updates/sec

Title: US-09-784-810C-1

Perfect score: 1600

Sequence: 1 nccccccggggtccctatag.....aaataagtgacattcccaa 1600

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/2/ina/PCUTUS_COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Query length | DB ID | Description |
|------------|--------|-------------|--------------|-------|---------------------------------------|
| 1 | 1426.8 | 89.2 | 1533 | 4 | US-09-205-258-90 Sequence 90, Appl |
| 2 | 1124.6 | 70.3 | 1155 | 4 | US-09-970-516-1 Sequence 1, Appl |
| 3 | 742.4 | 46.4 | 1149 | 4 | US-09-970-516-5 Sequence 5, Appl |
| 4 | 258 | 16.1 | 1857 | 4 | US-09-970-516-3 Sequence 3, Appl |
| 5 | 49.6 | 3.1 | 1203 | 3 | US-09-086-010-1 Sequence 1, Appl |
| 6 | 48.6 | 3.0 | 4403765 | 3 | US-09-103-840A-2 Sequence 2, Appl |
| 7 | 47.8 | 3.0 | 900 | 5 | PCT-US95-04801-3 Sequence 3, Appl |
| 8 | 47.2 | 3.0 | 2793 | 1 | US-08-458-298-1 Sequence 1, Appl |
| 9 | 47.2 | 3.0 | 2793 | 1 | US-08-458-298-1 Sequence 1, Appl |
| 10 | 47 | 2.9 | 68750 | 3 | US-09-335-409-1 Sequence 1, Appl |
| 11 | 47 | 2.9 | 68750 | 4 | US-09-568-102-1 Sequence 1, Appl |
| 12 | 47 | 2.9 | 68750 | 4 | US-09-567-969-1 Sequence 1, Appl |
| 13 | 47 | 2.9 | 68750 | 4 | US-09-568-480-1 Sequence 1, Appl |
| 14 | 47 | 2.9 | 68750 | 4 | US-09-568-486-1 Sequence 1, Appl |
| 15 | 47 | 2.9 | 68750 | 4 | US-09-568-472-1 Sequence 1, Appl |
| 16 | 47 | 2.9 | 68750 | 4 | US-09-567-899-1 Sequence 1, Appl |
| 17 | 46.6 | 2.9 | 2011 | 6 | 5256770 Patent No. 5256770 |
| 18 | 46.4 | 2.9 | 993 | 4 | US-09-252-991A-2002 Sequence 2002, Ap |
| 19 | 46.4 | 2.9 | 1221 | 4 | US-09-252-991A-2160 Sequence 2160, Ap |
| 20 | 46.4 | 2.9 | 1269 | 4 | US-09-252-991A-2089 Sequence 2089, Ap |
| 21 | 46.4 | 2.9 | 1482 | 4 | US-09-252-991A-1723 Sequence 1723, Ap |
| 22 | 46.4 | 2.9 | 1506 | 4 | US-09-252-991A-1875 Sequence 1875, Ap |
| 23 | 46.4 | 2.9 | 53526 | 3 | US-08-658-136-2 Sequence 2, Appl |
| 24 | 46.4 | 2.9 | 53527 | 3 | US-08-658-136-1 Sequence 1, Appl |
| 25 | 45.2 | 2.8 | 918 | 4 | US-09-252-991A-1131 Sequence 1131, Ap |
| 26 | 45.2 | 2.8 | 1338 | 4 | US-09-252-991A-1058 Sequence 1058, Ap |
| 27 | 45 | 2.8 | 441529 | 3 | US-09-103-840A-1 Sequence 1, Appl |

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| 28 | 44.8 | 2.8 | 1164 | 1 | US-07-640-476-6 Sequence 6, Appl |
| 29 | 44.8 | 2.8 | 1614 | 4 | US-09-616-289-45 Sequence 45, Appl |
| 30 | 44.8 | 2.8 | 12425 | 4 | US-08-616-289-50 Sequence 50, Appl |
| 31 | 44.6 | 2.8 | 4257 | 2 | US-08-630-473-1 Sequence 1, Appl |
| 32 | 44.6 | 2.8 | 4257 | 3 | US-09-259-821A-1 Sequence 1, Appl |
| 33 | 44.6 | 2.8 | 4257 | 3 | US-08-843-659-1 Sequence 1, Appl |
| 34 | 44.6 | 2.8 | 12001 | 1 | US-08-458-568A-11 Sequence 11, Appl |
| 35 | 44.4 | 2.8 | 759 | 4 | US-09-252-991A-1802 Sequence 1802, Ap |
| 36 | 44.2 | 2.8 | 1119 | 4 | US-09-252-991A-13765 Sequence 13765, A |
| 37 | 44.2 | 2.8 | 2349 | 4 | US-08-252-991A-13765 Sequence 13765, A |
| 38 | 44.2 | 2.8 | 3081 | 4 | US-09-252-991A-13660 Sequence 13660, A |
| 39 | 44.2 | 2.8 | 4403765 | 3 | US-09-103-840A-2 Sequence 2, Appl |
| 40 | 43.8 | 2.7 | 71989 | 4 | US-09-443-501A-2 Sequence 2, Appl |
| 41 | 43.4 | 2.7 | 505 | 4 | US-09-621-976-15639 Sequence 15639, A |
| 42 | 43.4 | 2.7 | 1921 | 3 | US-08-482-677-3 Sequence 3, Appl |
| 43 | 43.4 | 2.7 | 1921 | 4 | US-10-033-174-3 Sequence 3, Appl |
| 44 | 43.4 | 2.7 | 1926 | 1 | US-08-152-019A-43 Sequence 43, Appl |
| 45 | 43.2 | 2.7 | 759 | 4 | US-09-252-991A-9217 Sequence 9217, Ap |

ALIGNMENTS

RESULT 1
US-09-205-258-90
Sequence 90, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06

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 QY 1309 ACCGCGAGAGAGCCCTATGACCCCTGGCGCGCTGTGCTTATGTTACTTGACG 1358
 Db 1207 ACCGCGAGAGAGCCCTATGACCCCTGGCGCGCTGTGCTTATGTTACTTGACG 1266
 QY 1369 ACCCTTCCCTCCCTCAAGGCTGAGGAGCTGTGCTCAAGCTCTGTGGGAGAGAG 1428
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 QY 1429 ACTCTCTGAGAGAGGCTGAGAGGCTGAGGCTTGTGGGAGAGAGAGGCTGAGAG 1488
 Db 1387 ACTCTCTGAGAGAGGCTGAGAGGCTGAGGCTTGTGGGAGAGAGAGGCTGAGAG 1386
 QY 1489 AGTCTGGGTGAGAGCCAGCTGGCTGGCCCACTGCTATGTAAGGCTTGTAGTT 1548
 Db 1387 AGTCTGGGTGAGAGCCAGCTGGCTGGCCCACTGCTATGTAAGGCTTGTAGTT 1446
 QY 1549 GTTCTGAGAGCCCAAGCCCAAGCAATCCAAATGAAGTGAATTCCCA 1600
 Db 1447 GTTCTGAGAGCCCAAGCCCAAGCAATCCAAATGAAGTGAATTCCCA 1498

RESULT 2

US-09-970-516-1
 ; Sequence 1, Application US/09970516
 ; Patent No. 6610534
 ; GENERAL INFORMATION:
 ; APPLICANT: No. 6610534artis AG
 ; TITLE OF INVENTION: Induction of blood vessel formation through administration of
 ; FILE OF INVENTION: polynucleotides encoding sphingosine kinases
 ; FILE REFERENCE: 4-31617
 ; CURRENT APPLICATION NUMBER: US/09/970,516
 ; CURRENT FILING DATE: 2001-10-04
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 1
 ; LENGTH: 1155
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1155)
 ; OTHER INFORMATION:
 US-09-970-516-1

Query Match 70.3%; Score 1124.6; DB 4; Length 1155;
 Best Local Similarity 98.4%; Pred. No. 1.6e-248;
 Matches 1136; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 176 ATGATTCAGCGGCGCGCCCGGGGCTGCTCCCGCGGCTGCTGCTGCTGCTGCTG 235
 Db 1 ATGATTCAGCGGCGGCGCGCCCGGGGCTGCTCCCGCGGCTGCTGCTGCTGCTG 60
 QY 236 CTGAACCCGCGCGGCGGCAAGGAGGCTTGCAGCTCTTCCGAGTCAAGTGAAGCC 295
 Db 61 CTGAACCCGCGCGGCGGCAAGGAGGCTTGCAGCTCTTCCGAGTCAAGTGAAGCC 120
 QY 236 CTTTGGCTGAGGCTGAATCTCTTCAAGCTGATGCTCACTGAGCGGAGCAACGCG 355
 Db 121 CTTTGGCTGAGGCTGAATCTCTTCAAGCTGATGCTCACTGAGCGGAGCAACGCG 180
 QY 356 CGGAGCTGCTGCTGCTGAGAGAGCTGGCGCTGGAGAGCTGCTGCTGCTGCTGCTG 415
 Db 181 CGGAGCTGCTGCTGCTGAGAGAGCTGGCGCTGGAGAGCTGCTGCTGCTGCTGCTG 240
 QY 416 GACGGGCTGATGCAAGAGTGTGAGACGGGCTCATGAGCGGCTGACTGGAGAGCCGC 475
 Db 241 GACGGGCTGATGCAAGAGTGTGAGACGGGCTCATGAGCGGCTGACTGGAGAGCCGC 300
 QY 476 ATCCGAAGCCCTCTGTGAGCTCCAGAGAGCTCTGGCAAGCGGCTGGCAAGCTTCTG 535
 Db 301 ATCCGAAGCCCTCTGTGAGCTCCAGAGAGCTCTGGCAAGCGGCTGGCAAGCTTCTG 360

QY 536 AACCATTAAGCTGGCTATGAGCAGGTCAACCAATGAAGAGCTCTCTGACCACTGACAGCTA 595
 Db 361 AACCATTAAGCTGGCTATGAGCAGGTCAACCAATGAAGAGCTCTCTGACCACTGACAGCTA 420
 QY 596 TTGCTGAGCGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 655
 Db 421 TTGCTGAGCGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 656 CTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 715
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 QY 716 AGTATTAAGTATGAGGCTGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 775
 Db 541 AGTATTAAGTATGAGGCTGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 QY 776 GCAAGCTGCGCACTTACCGCGGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 835
 Db 601 GCAAGCTGCGCACTTACCGCGGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 836 AAGACACTGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 895
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 QY 896 CTGAGAGAGAGGCTGCTTCTCACTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 955
 Db 721 CTGAGAGAGAGGCTGCTTCTCACTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 956 CTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1015
 Db 781 CTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 1016 GCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
 Db 841 GCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 1076 CGCCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1135
 Db 901 CGCCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 1136 TATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1195
 Db 961 TATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
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 Db 1021 GATGAGGAATTGATGCTGAGCGAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAG 1080
 QY 1256 ATGCTCAGCGCTGCTGAGAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1315
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 QY 1316 GAAGAGCCCTATGA 1330
 Db 1141 GAAGAGCCCTATGA 1155

RESULT 3

US-09-970-516-5
 ; Sequence 5, Application US/09970516
 ; Patent No. 6610534
 ; GENERAL INFORMATION:
 ; APPLICANT: No. 6610534artis AG
 ; TITLE OF INVENTION: Induction of blood vessel formation through administration of
 ; FILE OF INVENTION: polynucleotides encoding sphingosine kinases
 ; FILE REFERENCE: 4-31617
 ; CURRENT APPLICATION NUMBER: US/09/970,516
 ; CURRENT FILING DATE: 2001-10-04
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 5
 ; LENGTH: 1149

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| Db | 1511 | GGTCAAGGTGATTCACGGTGC | CCGAGCAGAGACTGATGCTGCTGCACAGCTGTGCAACAGAG | 1570 |
| Qy | 391 | GGACGCTCTGGTGTGCATGCTG | AGAGACGGGCTGATGCACAGAGGTGGGAAACGGGCTCAT | 450 |
| Db | 1571 | GCCGAGAGCGCTGATGCTTACG | GTACAGAGTCTGATCTGAGACCTGGTCCCGCTGCTGAGG | 1630 |
| Qy | 451 | GGAGCGGC | 458 | |
| Db | 1631 | GCAGGTGC | 1638 | |

RESULT 9
US-08-458-298-1

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; GENERAL INFORMATION:
; APPLICANT: Lewis, Randolph V.

```

```

; TITLE OF INVENTION:  cDNAs Encoding Minor Ampullate Spider
; TITLE OF INVENTION:  Silk Proteins
; NUMBER OF SENTENCES:  6

```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEES: Birch, Stewart, Kolasch & Birch
; STREET: P O Box 747
; CITY: P O Box 747
; STATE: P O Box 747
; COUNTRY: P O Box 747

ZIP: 22040-3487
COMPUTER READABLE FORM:

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; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,747

OTHER INFORMATION: ampullate silk protein"

[illegible]

RESULT 10
US-09-335-409-1
; Sequence 1, Application US/09335409

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| Best Local Similarity | 47.0% | Pred. No. 0.26 | | |
| Matches 178 | Conservative | 0 | Mismatches 200 | Indels 1 |
| | | | Gaps | 1 |

Query Match 2.9%; Score 47; DB 4; Length 68750;
Best Local Similarity 47.0%; Pred. No. 0.26;
Matches 178; Conservative 0; Mismatches 200; Indels 1; Gaps 1;

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DB 56200 GCCGTGCGCGCGGCGGCGCGACCGCGCTTCGGGGGTGAGCGCTTCGCGCTCAGCGG 56259
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DB 56260 CACCAACGTCCATGTCTGTGTGAGAGCGCGCGCGCAGGTCTGCGACCGCGCAGCGCC 56319
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DB 56440 GTTCAGCTGTGTATCGACCGGTAAGCCCGATGAGACACCGGCTGCGGTGCGCGACCTC 56499
QY 319 CTTACGCTGATGCTCACTAGCGCGGAAACCAAGCGCGAGCTGTGCGTGTGAGAGA 378
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US-09-568-486-1
; Sequence 1, Application US/09568486
; Patent No. 6355459
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,486
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-486-1

Query Match 2.9%; Score 47; DB 4; Length 68750;
Best Local Similarity 47.0%; Pred. No. 0.26;
Matches 178; Conservative 0; Mismatches 200; Indels 1; Gaps 1;

QY 20 GCCACGCTCCCGGCGGGAGGCGAGCCCGACAGCGCGCCCTGCG-ACGCCCGCTGGG 78
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QY 79 CAGCACCAGTAAGAGACTGAAGCGACAGAGCCCGCGCAGCGGCGCCCGCCACAGCGCC 138
DB 56260 CACCAACGTCCATGTCTGTGTGAGAGCGCGCGCGCAGGTCTGCGACCGCGCAGCGCC 56319
QY 139 AGGAGACCCCTGCGCAGCGGAGCGCGGCTGAGTTATGATTCACAGCGGCGCGCCCG 198
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DB 56380 GGGCGCGCGCTCTCAGCGCACATCGCGCGTACCGCGAGCAGGCTCTGGAAGAGTGC 56439
QY 259 CAGGCGCTTGCAGCTCTTCCGAGTACAGTGCAGCCCGCTTTTGGCTGAGGCTGAATCTC 318
DB 56440 GTTCAGCTGTGTATCGACCGGTAAGCCCGATGAGACACCGGCTGCGGTGCGCGACCTC 56499
QY 319 CTTACGCTGATGCTCACTAGCGCGGAAACCAAGCGCGGAGCTGTGCGTGTGAGAGA 378
DB 56500 GCGCGAGCGCTGTGAAAGCGCGCTGTGAGGTTGCGCGCAGAGGCGACCCCGGAGCGC 56559
QY 379 GCTGGGCGCTGTGGAGCT 397
DB 56560 GCGCGCGCGCAGGCGCGCT 56578

QY 199 GGGCGTCTCCCGGCGGCGCTGCGCGCTGTGTCTGTGAACCCCGCGCGCGCAAGG 258
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RESULT 15
US-09-568-472-1
; Sequence 1, Application US/09568472
; Patent No. 6358719
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,472
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-472-1

Query Match 2.9%; Score 47; DB 4; Length 68750;
Best Local Similarity 47.0%; Pred. No. 0.26;
Matches 178; Conservative 0; Mismatches 200; Indels 1; Gaps 1;

QY 20 GCCACGCTCCCGGCGGGAGGCGAGCCCGACAGCGCGCCCTGCG-ACGCCCGCTGGG 78
DB 56200 GCCGTGCGCGCGGCGGCGGACCGCGCTTCGGGGGTGAGCGCTTCGCGCTCAGCGG 56259
QY 79 CAGCACCAGTAAGAGACTGAAGCGAGAGCGCGCGCGCCCGCCACAGCGCC 138
DB 56260 CACCAACGTCCATGTCTGTCTGTGAGAGAGCGCGCGCGCAGGTCTGCGACCGCGCAGCGCC 56319
QY 139 AGGAGACCCCTGCGCAGCGGAGCGCGGCTGAGTTATGATTCAGCGGCGCGCCCG 198
DB 56320 GGGGCGCTCAGCGGACCTTTTGTGTCTGTGTGCGGAAAGAGCGCGCGCTGGAAGACA 56379
QY 199 GGGCGTCTCCGCGGCGCCCTGCGCGCTGCTGTCTGTAAACCGCGCGCGCGCAAGG 258
DB 56380 GGGCGCGCGCTCTCAGCGCACATCGCGCGTACCGCGAGCAGGCTCTGGAAGAGTGC 56439
QY 259 CAGGCGCTTGCAGCTCTTCCGAGTACAGTGCAGCCCGCTTTTGGCTGAGGCTGAATCTC 318
DB 56440 GTTCAGCTGTGTATCGACCGGTAAGCCCGATGAGACACCGGCTGCGGTGCGCGACCTC 56499
QY 319 CTTACGCTGATGCTCACTAGCGCGGAAACCAAGCGCGGAGCTGTGCGTGTGAGAGA 378
DB 56500 GCGCGAGCGCTGTGAAAGCGCGCTGTGAGGTTGCGCGCAGAGGCGACCCCGGAGCGC 56559
QY 379 GCTGGGCGCTGTGGAGCT 397
DB 56560 GCGCGCGCGCAGGCGCGCT 56578

Mon Mar 1 09:38:57 2004

us-09-784-810c-1.rml

Page 10

Db 56560 GCGCGCGCGAGGCGCT 56578

Search completed: February 27, 2004, 09:46:05
Job time : 155 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 27, 2004, 09:46:12 ; Search time 569 Seconds

(without alignments)
10144.019 Million cell updates/sec

Title: US-09-784-810C-1

Perfect score: 1600

Sequence: 1 nccccccggggctccctataag.....aataaagtcacattcccaa 1600

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2353733 seqs, 180373377 residues

Total number of hits satisfying chosen parameters: 4707466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|--------|-------------|-----------|----|--------------------|
| 1 | 1599 | 99.9 | 1600 | 9 | US-09-784-810A-1 |
| 2 | 1560.6 | 97.5 | 1799 | 14 | US-10-354-358-25 |
| 3 | 1426.8 | 89.2 | 1533 | 10 | US-09-933-767-90 |
| 4 | 1426.8 | 89.2 | 1533 | 14 | US-10-023-282-90 |
| 5 | 1387.2 | 86.7 | 1562 | 15 | US-10-264-237-1180 |
| 6 | 1124.6 | 70.3 | 1155 | 9 | US-09-970-516-1 |
| 7 | 1120 | 70.0 | 1152 | 15 | US-10-348-052-22 |
| 8 | 836.4 | 52.3 | 1759 | 9 | US-09-784-810A-3 |
| 9 | 742.4 | 46.4 | 1149 | 9 | US-09-970-516-5 |
| 10 | 382.6 | 23.9 | 394 | 9 | US-09-954-456-1756 |
| 11 | 286.6 | 17.9 | 480 | 9 | US-09-783-590-9248 |
| 12 | 258 | 16.1 | 1857 | 9 | US-09-970-516-3 |
| 13 | 258 | 16.1 | 2380 | 9 | US-09-817-676A-13 |
| 14 | 258 | 16.1 | 2380 | 14 | US-10-354-358-77 |
| 15 | 242 | 15.1 | 2698 | 9 | US-09-817-676A-11 |

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| 16 | 197.4 | 12.3 | 199 | 9 | US-09-796-692-2905 | Sequence 2905, Ap |
| 17 | 197.4 | 12.3 | 199 | 14 | US-10-040-862-2905 | Sequence 2905, Ap |
| 18 | 197.4 | 12.3 | 199 | 15 | US-10-057-475B-2905 | Sequence 2905, Ap |
| 19 | 197.4 | 12.3 | 199 | 15 | US-10-154-884B-2905 | Sequence 2905, Ap |
| 20 | 193 | 12.1 | 296 | 9 | US-09-777-564-658 | Sequence 658, App |
| 21 | 193 | 12.1 | 296 | 14 | US-10-015-219-658 | Sequence 658, App |
| 22 | 176.8 | 11.1 | 585 | 15 | US-10-027-632-196470 | Sequence 196470, A |
| 23 | 117.8 | 7.4 | 428 | 15 | US-10-191-803-456 | Sequence 456, App |
| 24 | 114.4 | 7.2 | 832 | 14 | US-10-029-386-20952 | Sequence 20952, A |
| 25 | 114.4 | 7.2 | 1394 | 15 | US-10-264-049-204 | Sequence 204, App |
| 26 | 102 | 6.4 | 507 | 14 | US-10-029-386-7252 | Sequence 7252, Ap |
| 27 | 97 | 6.1 | 2609 | 15 | US-10-348-052-25 | Sequence 25, Appl |
| 28 | 87.4 | 5.5 | 1869 | 12 | US-10-425-114-3806 | Sequence 34806, A |
| 29 | 83.4 | 5.2 | 2639 | 15 | US-10-348-052-24 | Sequence 427396, A |
| 30 | 64.6 | 4.0 | 2084 | 12 | US-10-424-599-43396 | Sequence 14378, A |
| 31 | 60 | 3.8 | 60 | 10 | US-09-908-975-14378 | Sequence 25926, A |
| 32 | 53.8 | 3.4 | 732 | 14 | US-10-259-165-115 | Sequence 115, App |
| 33 | 52 | 3.2 | 7185 | 14 | US-10-282-122A-25926 | Sequence 48, Appl |
| 34 | 52 | 3.2 | 6194 | 14 | US-10-329-079-34 | Sequence 34, Appl |
| 35 | 52 | 3.2 | 2136 | 14 | US-10-156-761-7476 | Sequence 7476, Ap |
| 36 | 51.8 | 3.2 | 3135 | 14 | US-10-156-761-5936 | Sequence 5936, Ap |
| 37 | 51.8 | 3.2 | 51657 | 15 | US-10-057-475B-10475 | Sequence 10475, A |
| 38 | 51.8 | 3.2 | 51657 | 15 | US-10-154-884B-10475 | Sequence 10475, A |
| 39 | 51.8 | 3.2 | 9025608 | 14 | US-10-156-761-1 | Sequence 1, Appl |
| 40 | 51.8 | 3.2 | 9025608 | 14 | US-10-156-761-1 | Sequence 1, Appl |
| 41 | 51.8 | 3.2 | 1614 | 10 | US-09-969-896-16 | Sequence 16, Appl |
| 42 | 51.2 | 3.2 | 4413 | 10 | US-09-969-896-16 | Sequence 16, Appl |
| 43 | 51.2 | 3.2 | 4413 | 10 | US-10-120-988-148 | Sequence 148, App |
| 44 | 51.2 | 3.2 | 4463 | 14 | US-10-315-597A-1 | Sequence 1, Appl |
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ALIGNMENTS

RESULT 1

US-09-784-810A-1

Sequence 1, Application US/09784810A

Patent No. US20020082203A1

GENERAL INFORMATION:

APPLICANT: RASTELLI, LUCA

TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING

TITLE OF INVENTION: SAME

FILE REFERENCE: 10746-08

CURRENT APPLICATION NUMBER: US/09/784, 810A

CURRENT FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/182,360

PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: 60/191,261

PRIOR FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1600

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: modified_base

LOCATION: (1)

OTHER INFORMATION: a, t, c, g, other or unknown

US-09-784-810A-1

Query Match 99.9%; Score 1599; DB 9; Length 1600;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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2 TGGGACCGCCGCTGGGACAGCAGCTTAAAGGAGAGAGAGAGAGAGAGAGAGAGAG 121

62 TGGGACCGCCGCTGGGACAGCAGCTTAAAGGAGAGAGAGAGAGAGAGAGAGAGAG 121

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 122

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 25

LENGTH: 1799

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (359)...(1513)

S-10-354-358-25

Query Match 97.5%; Score 1560.6; DB 14; Length 1799;

Best Local Similarity 98.4%; Pred No. 0;

Matches 1572; Conservative 3; Mismatches 22; Indels 0; Gaps 0;

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| b | 187 | CGCCGGTCTCTACAGCAGCGGCTCCGGCGGGGAGCGAGCCACACCGCCCTG | 246 |
| y | 64 | CGACCCCGCTGGGACAGCAGGATAGGAGCTGAAGGAGCGCGCCACCGGCAG | 123 |
| b | 247 | CGACCCCGCTGGGACAGCAGGATAGGAGCTGAAGGAGCGCGCCACCGGCAG | 306 |
| y | 124 | CGCCCCACAGCCAGGAGCCCTTGGCAGCGGAGCGCGGTCGAGGTTATGGATCC | 183 |
| b | 307 | CGCCCCACAGCCAGGAGCCCTTGGCAGCGGAGCGCGGTCGAGGTTATGGATCC | 366 |
| y | 184 | AGCGGGCGCCCGGGCGTGTCTCCCGGCGCTCCCGGCTGTGTGTGTGTGTGT | 243 |
| b | 367 | AGCGGGCGCCCGGGCGTGTCTCCCGGCGCTCCCGGCTGTGTGTGTGTGTGT | 426 |
| y | 244 | GGCGGGCGGCAAGGCGAGGCTTTCAGCTCTTCCGAGTCACTGACGCGCCCTTTGGC | 303 |
| b | 427 | GGCGGGCGGCAAGGCGAGGCTTTCAGCTCTTCCGAGTCACTGACGCGCCCTTTGGC | 486 |
| y | 304 | TGAGGCTGAATCTCTCTTCACTGATGCTCACTGAGCGGCGGAGACACGCGGGAGCT | 363 |
| b | 487 | TGAGGCTGAATCTCTCTTCACTGATGCTCACTGAGCGGCGGAGACACGCGGGAGCT | 546 |
| y | 364 | GGTGGGTCGAGGAGCTGGGCGCTGGAGCTCTGGTGTGTGTGTGTGTGTGTGTGT | 423 |
| b | 547 | GGTGGGTCGAGGAGCTGGGCGCTGGAGCTCTGGTGTGTGTGTGTGTGTGTGTGT | 606 |
| y | 424 | GATGACAGGTCGTGAACGGGCTCATGAGCGGCTCACTGAGGAGCGCCATCCAGAA | 483 |
| b | 607 | GATGACAGGTCGTGAACGGGCTCATGAGCGGCTCACTGAGGAGCGCCATCCAGAA | 666 |
| y | 484 | GGCCCTGTGTAGCTCCAGCAGGCTTGGCAACGCGTGGAGCTTCTTGAACCATTA | 543 |
| b | 667 | GGCCCTGTGTAGCTCCAGCAGGCTTGGCAACGCGTGGAGCTTCTTGAACCATTA | 726 |
| y | 544 | TGCTGGCTATGAGCAGGTACCAATGAAGACCTCTGACCACTGACGCTATTGCTGTG | 603 |
| b | 727 | TGCTGGCTATGAGCAGGTACCAATGAAGACCTCTGACCACTGACGCTATTGCTGTG | 786 |
| y | 604 | CGCCCGGTGTGTACCCATGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 663 |
| b | 787 | CGCCCGGTGTGTACCCATGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 846 |
| y | 664 | GTCTCTGT | 723 |
| b | 847 | GTCTCTGT | 906 |
| y | 724 | GTATCGGCTGTGGGGAGATGCGCTTCACTGTGGGCACTTCTGTGTGTGTGTGTGT | 783 |
| b | 907 | GTATCGGCTGTGGGGAGATGCGCTTCACTGTGGGCACTTCTGTGTGTGTGTGTGT | 966 |
| y | 784 | GGGCACTTACCGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 843 |
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| y | 844 | TGCTTCCCCCTGT | 903 |

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| Db | 1027 | TGCTTCCCCCTGT | 1086 |
| Qy | 904 | GCAGTGCCTTCTCACTGCGAGGTGTGCCCGACGAGGACTTTGTGTGTGTGTGTGT | 963 |
| Db | 1087 | GCAGTGCCTTCTCACTGCGAGGTGTGCCCGACGAGGACTTTGTGTGTGTGTGTGT | 1146 |
| Qy | 964 | GCTGCACTCGCACTTGGCGGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 1023 |
| Db | 1147 | GCTGCACTCGCACTTGGCGGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 1206 |
| Qy | 1024 | CGTATGCACTTGTCTTACGTGCGGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGT | 1083 |
| Db | 1207 | CGTATGCACTTGTCTTACGTGCGGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGT | 1266 |
| Qy | 1084 | CTTGGCCATGAGAGGCGGAGCATATGAGTATGATGATGATGATGATGATGATGAT | 1143 |
| Db | 1267 | CTTGGCCATGAGAGGCGGAGCATATGAGTATGATGATGATGATGATGATGATGAT | 1326 |
| Qy | 1144 | CGTGTGTGCTTCCGCTTGGAGCCCAAGGATGGAAAGTGTGTGTGTGTGTGTGTGT | 1203 |
| Db | 1327 | CGTGTGTGCTTCCGCTTGGAGCCCAAGGATGGAAAGTGTGTGTGTGTGTGTGTGT | 1386 |
| Qy | 1204 | ATTGATGTTAGGAGCGCGTGCAGGCGGAGGTGTGTGTGTGTGTGTGTGTGTGTGT | 1263 |
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| Db | 1447 | CGTTCGCTGGAGCGCCCGCCAGCTGGAAGCCCGCAGAGATGCCACCGCCAGAGGCC | 1506 |
| Qy | 1324 | CTTATGACCCCTGGGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 1383 |
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| Qy | 1444 | GGTGAGAGGTGAGGCTATGCTTTGGGGGACAGCCAGAGATGAAAGTCTTGGGTGAG | 1503 |
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| Qy | 1504 | GCCAGCTGCTGGGCGGAGCTGTCTTATGAGGCTTCTAGTTGTTCTGAGACCCCA | 1563 |
| Db | 1687 | GCCAGCTGCTGGGCGGAGCTGTCTTATGAGGCTTCTAGTTGTTCTGAGACCCCA | 1746 |
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RESULT 3

US-09-933-767-90

Sequence 90, Application US/09933767

Publication No. US20030181692A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: 207 Human Secreted Proteins

FILE REFERENCE: P2007P2

CURRENT APPLICATION NUMBER: US/09/933,767

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: PCT/US01/05614

PRIOR FILING DATE: 2001-02-21

PRIOR APPLICATION NUMBER: 60/184,836

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 60/193,170

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 09/205,258

PRIOR FILING DATE: 1998-12-04

PRIOR APPLICATION NUMBER: PCT/US98/11422

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/048,885

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| 1 | PRIOR FILING DATE: | 1997-06-06 |
| 2 | PRIOR APPLICATION NUMBER: | 60/049,375 |
| 3 | PRIOR FILING DATE: | 1997-06-06 |
| 4 | PRIOR APPLICATION NUMBER: | 60/048,881 |
| 5 | PRIOR FILING DATE: | 1997-06-06 |
| 6 | PRIOR APPLICATION NUMBER: | 60/048,880 |
| 7 | PRIOR FILING DATE: | 1997-06-06 |
| 8 | PRIOR APPLICATION NUMBER: | 60/048,896 |
| 9 | PRIOR FILING DATE: | 1997-06-06 |
| 10 | PRIOR APPLICATION NUMBER: | 60/049,020 |
| 11 | PRIOR FILING DATE: | 1997-06-06 |
| 12 | PRIOR APPLICATION NUMBER: | 60/048,876 |
| 13 | PRIOR FILING DATE: | 1997-06-06 |
| 14 | PRIOR APPLICATION NUMBER: | 60/048,895 |
| 15 | PRIOR FILING DATE: | 1997-06-06 |
| 16 | PRIOR APPLICATION NUMBER: | 60/048,884 |
| 17 | PRIOR FILING DATE: | 1997-06-06 |
| 18 | PRIOR APPLICATION NUMBER: | 60/048,894 |
| 19 | PRIOR FILING DATE: | 1997-06-06 |
| 20 | PRIOR APPLICATION NUMBER: | 60/048,971 |
| 21 | PRIOR FILING DATE: | 1997-06-06 |
| 22 | PRIOR APPLICATION NUMBER: | 60/048,964 |
| 23 | PRIOR FILING DATE: | 1997-06-06 |
| 24 | PRIOR APPLICATION NUMBER: | 60/048,882 |
| 25 | PRIOR FILING DATE: | 1997-06-06 |
| 26 | PRIOR APPLICATION NUMBER: | 60/048,899 |
| 27 | PRIOR FILING DATE: | 1997-06-06 |
| 28 | PRIOR APPLICATION NUMBER: | 60/048,893 |
| 29 | PRIOR FILING DATE: | 1997-06-06 |
| 30 | PRIOR APPLICATION NUMBER: | 60/048,900 |
| 31 | PRIOR FILING DATE: | 1997-06-06 |
| 32 | PRIOR APPLICATION NUMBER: | 60/048,901 |
| 33 | PRIOR FILING DATE: | 1997-06-06 |
| 34 | PRIOR APPLICATION NUMBER: | 60/048,892 |
| 35 | PRIOR FILING DATE: | 1997-06-06 |
| 36 | PRIOR APPLICATION NUMBER: | 60/048,915 |
| 37 | PRIOR FILING DATE: | 1997-06-06 |
| 38 | PRIOR APPLICATION NUMBER: | 60/049,019 |
| 39 | PRIOR FILING DATE: | 1997-06-06 |
| 40 | PRIOR APPLICATION NUMBER: | 60/048,970 |
| 41 | PRIOR FILING DATE: | 1997-06-06 |
| 42 | PRIOR APPLICATION NUMBER: | 60/048,972 |
| 43 | PRIOR FILING DATE: | 1997-06-06 |
| 44 | PRIOR APPLICATION NUMBER: | 60/048,916 |
| 45 | PRIOR FILING DATE: | 1997-06-06 |
| 46 | PRIOR APPLICATION NUMBER: | 60/049,373 |
| 47 | PRIOR FILING DATE: | 1997-06-06 |
| 48 | PRIOR APPLICATION NUMBER: | 60/048,875 |
| 49 | PRIOR FILING DATE: | 1997-06-06 |
| 50 | PRIOR APPLICATION NUMBER: | 60/049,374 |
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| 52 | PRIOR APPLICATION NUMBER: | 60/048,917 |
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| 54 | PRIOR APPLICATION NUMBER: | 60/048,949 |
| 55 | PRIOR FILING DATE: | 1997-06-06 |
| 56 | PRIOR APPLICATION NUMBER: | 60/048,974 |
| 57 | PRIOR FILING DATE: | 1997-06-06 |
| 58 | PRIOR APPLICATION NUMBER: | 60/048,883 |
| 59 | PRIOR FILING DATE: | 1997-06-06 |
| 60 | PRIOR APPLICATION NUMBER: | 60/048,897 |
| 61 | PRIOR FILING DATE: | 1997-06-06 |
| 62 | PRIOR APPLICATION NUMBER: | 60/048,898 |
| 63 | PRIOR FILING DATE: | 1997-06-06 |
| 64 | PRIOR APPLICATION NUMBER: | 60/048,862 |
| 65 | PRIOR FILING DATE: | 1997-06-06 |
| 66 | PRIOR APPLICATION NUMBER: | 60/048,963 |
| 67 | PRIOR FILING DATE: | 1997-06-06 |
| 68 | PRIOR APPLICATION NUMBER: | 60/048,877 |
| 69 | PRIOR FILING DATE: | 1997-06-06 |
| 70 | PRIOR APPLICATION NUMBER: | 60/048,878 |
| 71 | PRIOR FILING DATE: | 1997-06-06 |
| 72 | PRIOR APPLICATION NUMBER: | 60/068,054 |
| 73 | PRIOR FILING DATE: | 1997-12-18 |

307 TYTGAGAGCGGCTGATGACGAGGTGGTGAACGGCTTCATGGAGCGCCTGACTGGGA 366
469 GACCGCATCCAGAGCCCTGTGTAGCTCCAGCAGGCTCTGCAACGCGCTGGCAGC 528
367 GACCGCATCCAGAGCCCTGTGTAGCTCCAGCAGGCTCTGCAACGCGCTGGCAGC 426
529 TTCCTTGAACCATTAATGCTGGCTATGAGCAGGTTCACCAATGAGACCTCTCAGCAACTG 588
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589 CACGCTATTGCTGTGCGGCGGCTGTGTACCCATGAACCTGTCTCTCTCAGCAAGC 648
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649 TTCGGGCTCGGCTCTCTCTGTGTGTGCTGAGCTGCGCTGGGCTTCATGCTGATGGA 708
547 TTCGGGCTCGGCTCTCTCTGTGTGTGCTGAGCTGCGCTGGGCTTCATGCTGATGGA 606
709 CTTAGAGAGTGAATGATGCGGCTGTGGGGAGATGCGCTTCACTCTGGGCACTTCT 768
607 CTTAGAGAGTGAATGATGCGGCTGTGGGGAGATGCGCTTCACTCTGGGCACTTCT 666
769 GCGTCTGGAGCGCTCGGCACTTACCGCGGCGGCTGAGCTACCTCTCTGTAGGAAGT 828
667 GCGTCTGGAGCGCTCGGCACTTACCGCGGCGGCTGAGCTACCTCTCTGTAGGAAGT 726
829 GCGTCTCAAGACACCTGCTTCCCGCTGTGTGTGCTGAGCAGGCGCGGTAGTGACACCT 888
727 GCGTCTCAAGACACCTGCTTCCCGCTGTGTGTGCTGAGCAGGCGCGGTAGTGACACCT 786
889 GGTGCGCACTGGAGGACGAGTGTCTCTCACTGGCAGGTGGTGGCGGAGGAGTGTGT 948
787 GGTGCGCACTGGAGGACGAGTGTCTCTCACTGGCAGGTGGTGGCGGAGGAGTGTGT 846
949 GGTGCGCACTGGAGGACGAGTGTCTCTCACTGGCAGGTGGTGGCGGAGGAGTGTGT 1008
847 GGTGCGCACTGGAGGACGAGTGTCTCTCACTGGCAGGTGGTGGCGGAGGAGTGTGT 906
1009 CCGCTGTGAGCTGGGCTCATGCTGTCTTACGTGCGGGGGGAGTGTCTCTGCGCAT 1068
907 CCGCTGTGAGCTGGGCTCATGCTGTCTTACGTGCGGGGGGAGTGTCTCTGCGCAT 966
1069 GCTGCTGGGCTCTTCTGGGCTATGAGAGGAGGAGGAGGAGTATGAGTATGAGTATG 1128
967 GCTGCTGGGCTCTTCTGGGCTATGAGAGGAGGAGGAGGAGTATGAGTATGAGTATG 1026
1129 CTTGCTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188
1027 CTTGCTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
1189 TGCACTGGATGGGAAATGATGCTTACGAGGCGGCTGAGGCGGCTGAGTATGAGTATG 1248
1087 TGCACTGGATGGGAAATGATGCTTACGAGGCGGCTGAGGCGGCTGAGTATGAGTATG 1146
1249 CTTGCTGATGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1308
1147 CTTGCTGATGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
1309 ACCGCGAGAGAGCCCTTATGACCCCTGGGCGGCTGTGCTGTAGTGTCTACTTGCAGG 1368
1207 ACCGCGAGAGAGCCCTTATGACCCCTGGGCGGCTGTGCTGTAGTGTCTACTTGCAGG 1266
1369 ACCCTTCT 1428
1267 ACCCTTCT 1326
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1327 ACTCTCTCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 1386
1489 AGTCTCTGGGTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 1548
1387 AGTCTCTGGGTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTTCTAGTTT 1446

OY 1549 GTTCTGAGACCCCGACCCCGACCGAACCAGAACCCAAATCCAAATTAAGTGACATTCCCAA 1600
Db 1447 GTTCTGAGACCCCGACCCCGACCGAACCAGAACCCAAATCCAAATTAAGTGACATTCCCAA 1498
RESULT 4
US-10-023-282-90
; Sequence 90, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
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; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917

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1  / EARLIER FILING DATE: 1997-06-06
2  / EARLIER APPLICATION NUMBER: 60/048,949
3  / EARLIER FILING DATE: 1997-06-06
4  / EARLIER APPLICATION NUMBER: 60/048,974
5  / EARLIER FILING DATE: 1997-06-06
6  / EARLIER APPLICATION NUMBER: 60/048,883
7  / EARLIER FILING DATE: 1997-06-06
8  / EARLIER APPLICATION NUMBER: 60/048,897
9  / EARLIER FILING DATE: 1997-06-06
10 / EARLIER APPLICATION NUMBER: 60/048,898
11 / EARLIER FILING DATE: 1997-06-06
12 / EARLIER APPLICATION NUMBER: 60/048,962
13 / EARLIER FILING DATE: 1997-06-06
14 / EARLIER APPLICATION NUMBER: 60/048,963
15 / EARLIER FILING DATE: 1997-06-06
16 / EARLIER APPLICATION NUMBER: 60/048,877
17 / EARLIER FILING DATE: 1997-06-06
18 / EARLIER APPLICATION NUMBER: 60/048,878
19 / EARLIER FILING DATE: 1997-06-06
20 / EARLIER APPLICATION NUMBER: 60/070,923
21 / EARLIER FILING DATE: 1997-12-18
22 / EARLIER APPLICATION NUMBER: 60/092,921
23 / EARLIER FILING DATE: 1998-07-15
24 / EARLIER APPLICATION NUMBER: 60/094,657
25 / EARLIER FILING DATE: 1998-07-30
26 / NUMBER OF SEQ ID NOS: 1227
27 / SOFTWARE: PatentIn Ver. 2.0
28 / SEQ ID NO 90
29 / LENGTH: 1533
30 / TYPE: DNA
31 / ORGANISM: Homo sapiens
32 / FEATURE:
33 / NAME/KEY: SITE
34 / LOCATION: (12)
35 / OTHER INFORMATION: n equals a,t,g, or c
36 / FEATURE:
37 / NAME/KEY: SITE
38 / LOCATION: (123)
39 / OTHER INFORMATION: n equals a,t,g, or c
40 / FEATURE:
41 / NAME/KEY: SITE
42 / LOCATION: (1522)
43 / OTHER INFORMATION: n equals a,t,g, or c
44 / FEATURE:
45 / NAME/KEY: SITE
46 / LOCATION: (1527)
47 / OTHER INFORMATION: n equals a,t,g, or c
48 / FEATURE:
49 / NAME/KEY: SITE
50 / LOCATION: (1527)
51 / OTHER INFORMATION: n equals a,t,g, or c
52 / US-10-023-282-90

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| Query Match | 89.2% | Score 1426.8 | DB 14 | Length 1533 |
|-----------------------|--------------|--------------|---------------|-------------|
| Best Local Similarity | 97.8% | Pred. No. 0 | | |
| Matches 1459 | Conservative | 6 | Mismatches 25 | Indels 2 |
| Gaps | | | | |
| QY | 110 | GC | GC | GC |
| DB | 8 | GC | GC | GC |
| QY | 170 | GAG | TT | AT |
| DB | 67 | GAG | TT | AT |
| QY | 230 | GTG | TG | CT |
| DB | 127 | GTG | TG | CT |
| QY | 290 | CAG | CC | CT |
| DB | 187 | CAG | CC | CT |
| QY | 350 | CAG | CG | CG |
| DB | 247 | CAG | CG | CG |

| | | | |
|----|------|--|------|
| Qy | 410 | TCGTGAGACGGGCTGATGACGAGGTGGTGAACGGGC-TCA TGGACGGGCTCACTGGGA | 468 |
| Db | 307 | TTTGGAGACGGGCTGATGACGAGGTGGTGAACGGGCTTCA TGGACGGGCTCACTGGGA | 366 |
| Qy | 469 | GACCGCATCCAGAACCCCTGTGTAGCCTCCAGCAGGCTCTGGCAAACGCGTGGCAGC | 528 |
| Db | 367 | GACCGCATCCAGAACCCCTGTGTAGCCTCCAGCAGGCTCTGGCAAACGCGTGGCAGC | 426 |
| Qy | 529 | TTCCCTTGAACCAATTATGCTGGCTATGAGCAGGTGACCAATGAAGACTCTCTGACCAACTG | 588 |
| Db | 427 | TTCCCTTGAACCAATTATGCTGGCTATGAGCAGGTGACCAATGAAGACTCTCTGACCAACTG | 486 |
| Qy | 589 | CAGCCTATTGCTGTGGCGCCGCTGTCTCACCATGAACCTGCTCTCTGTGCACACGGC | 648 |
| Db | 487 | CAGCCTATTGCTGTGGCGCGCTGTCTCACCATGAACCTGCTCTCTGTGCACACGGC | 546 |
| Qy | 649 | TTGGGGCTGCGCTCGTTCTCTGTGTCTACGCTGGCTGGGGTTTCA TTGCTGATGTGGA | 708 |
| Db | 547 | TTGGGGCTGCGCTCGTTCTCTGTGTCTACGCTGGCTGGGGTTTCA TTGCTGATGTGGA | 606 |
| Qy | 709 | CTTAGAGATGATAAGTATCGGGCTCTGGGGAGATGCGCTTCAC TCTGGGCACTTCCT | 768 |
| Db | 607 | CTTAGAGATGATAAGTATCGGGCTCTGGGGAGATGCGCTTCAC TCTGGGCACTTCCT | 666 |
| Qy | 769 | GGCTCTGGCAGCCCTCGCACCTACCGCGCCGAC TGGGTACCTCCCTGTAGGAAGT | 828 |
| Db | 667 | GGCTCTGGCAGCCCTCGCACCTACCGCGCCGAC TGGGTACCTCCCTGTAGGAAGT | 726 |
| Qy | 829 | GGGTTTCAAGACACCTGTTCCCGCTTGTGTCAGCAGGGCCGGTAGATGCACACCT | 888 |
| Db | 727 | GGGTTTCAAGACACCTGTCCTCCCGCTTGTGTCAGCAGGGCCGGTAGATGCACACCT | 786 |
| Qy | 889 | GGTGCCACTGGAGGACGAGTGCTTCTCACTGGCAGGTGTCGCCGAGCAGGACTTTGT | 948 |
| Db | 787 | TGTGCCACTGGAGGACGAGTGCCCTCTCACTGGA CAGTGGTGCCGACGAGACTTTGT | 846 |
| Qy | 949 | GCTAGTCTGGCACTGCTGTGA CTGCACTGGCCAGTGAGATGTTTTGCTGCACCCATGGG | 1008 |
| Db | 847 | GCTAGTCTGGCACTGCTGTGA CTGCACTGGCCAGTGAGATGTTTTGCTGCACCCATGGG | 906 |
| Qy | 1009 | CCGCTGTGACGTGGCGT CATGCATCTGTTTCTACGTGGCGGGAGTGCTCGTGCCAT | 1068 |
| Db | 907 | CCGCTGTGACGTGGCGT CATGCATCTGTTTCTACGTGGCGGGAGTGCTCGTGCCAT | 966 |
| Qy | 1069 | GCTGTGCGCTCTTCTGGCCATGGAAGGGCAGGCATATGGAGTATGAATGCCCTTA | 1128 |
| Db | 967 | GCTGTGCGCTCTTCTGGCCATGGAAGGGCAGGCATATGGAGTATGAATGCCCTTA | 1026 |
| Qy | 1129 | CTTGGTATATGTCGCCGTGCTCGCTTCGCTTGGAGCCCAAGGATGGGAAGSTGTGT | 1188 |
| Db | 1027 | CTTGGTATATGTCGCCGTGCTCGCTTCGCTTGGAGCCCAAGGATGGGAAGSTGTGT | 1086 |
| Qy | 1189 | TGCAGTGGATGGGAATTGATGTTTAGCAGGCCGTGACGGCCAGGTGCACCCAACTA | 1248 |
| Db | 1087 | TGCAGTGGATGGGAATTGATGTTTAGCAGGCCGTGACGGCCAGGTGCACCCAACTA | 1146 |
| Qy | 1249 | CTTCTGATGGTCAGCGTGTGGTGAGCCCCGCCAGCTGGAAGCCCCCAGAGATGCC | 1308 |
| Db | 1147 | CTTCTGATGGTCAGCGTGTGGTGAGCCCCGCCAGCTGGAAGCCCCCAGAGATGCC | 1206 |
| Qy | 1309 | ACCGCAGAGAAGCCCTTATGACCCCTGGGCCGCTGTGCCCTTAGTGTCTACTTGCAGG | 1368 |
| Db | 1207 | ACCGCAGAGAAGCCCTTATGACCCCTGGGCCGCTGTGCCCTTAGTGTCTACTTGCAGG | 1266 |
| Qy | 1369 | ACCTTCTCTTCCCTTAGGGCTGCAAGGCTGTGCCA CAGCTCCTGTGGGGGTGGAGGAG | 1428 |
| Db | 1267 | ACCTTCTCTTCCCTTAGGGCTGCAAGGCTGTGCCA CAGCTCCTGTGGGGGTGGAGGAG | 1326 |
| Qy | 1429 | ACTCCTCTGGAAGGGTGAGAGGTGGAGCTATGCTTTGGGGGACAGGCCAGCAATGA | 1488 |
| Db | 1327 | ACTCCTCTGGAAGGGTGAGAGGTGGAGCTATGCTTTGGGGGACAGGCCAGCAATGA | 1386 |
| Qy | 1489 | AGTCTCTGGGTACAGAGCCCACTGGCTGGGCCCAAGCTGCTATGTAAAGCCCTCTAGTTT | 1548 |

1387 AGTCCTGGGTACGAGCCAGCTGGCTGGGCCAGCTGCTATGTAGGCCCTTAGTTT 1446
1549 GTTCTGAGACCCCCACCAAGCAATCCAAATAAGTGACATTCCCAA 1600
1447 GTTCTGAGACCCCCACCAAGCAATCCAAATAAGTGACATTCCCAA 1498

RESULT 5

US-10-264-237-1180/c
Sequence 1180, Application US/10264237
Publication No. US2004000941A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P4131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1180
LENGTH: 1562
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (7)..(7)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (12)..(12)
OTHER INFORMATION: n equals a,t,g, or c
--10-264-237-1180

| Query Match | 86.7%; | Score 1387.2; | DB 15; | Length 1562; |
|-----------------------|--------------|--|----------------|-------------------|
| Best Local Similarity | 98.6%; | Pred. No. 0; | | |
| Matches 1398; | Conservative | 1; | Mismatches 19; | Indels 0; Gaps 0; |
| 183 | y | CAGCGGGCGCCCCCGGGCGTCTCCGCGGCCCTCGCGGCTGCTGCTGCTGCTGCAACC | 242 | |
| 1455 | b | CAGCGGGCGCCCCCGGGCGTCTCCGCGGCCCTCGCGGCTGCTGCTGCTGCTGCAACC | 1396 | |
| 243 | y | CGCGCGCGCGCAAGGCAAGGCGCTTTCGAGCTTTCCGAGTTCAGGTGACGTCGACCCCTTTTGG | 302 | |
| 1395 | b | CGCGCGCGCGCAAGGCAAGGCGCTTTCGAGCTTTCCGAGTTCAGGTGACGTCGACCCCTTTTGG | 1336 | |
| 303 | y | CTGAGGCTGAAATCTCTTCACGCTGATGCTCACTGACGCGCGGAAACACGCGCGGGAGC | 362 | |
| 1335 | b | CTGAGGCTGAAATCTCTTCACGCTGATGCTCACTGACGCGCGGAAACACGCGCGGGAGC | 1276 | |
| 363 | y | TGTTGCGGTCGGAGAGTGTGGCCGCTGGGACGCTCTGTTGTTCACTGTCTGGAGACGGGC | 422 | |
| 1275 | b | TGTTGCGGTCGGAGAGTGTGGCCGCTGGGACGCTCTGTTGTTCACTGTCTGGAGACGGGC | 1216 | |
| 423 | y | TGATGACAGAGTGTGTGAACGGGCTCATGAGCGGCTGTACTGGGAGACCGCCATCCAGA | 482 | |
| 1215 | b | TGATGACAGAGTGTGTGAACGGGCTCATGAGCGGCTGTACTGGGAGACCGCCATCCAGA | 1156 | |
| 483 | y | AGCCCCGTGTAGCCTCCGACGAGCTCTGGCAACGGCGCTGGCAGCTTCCTTGAAACATT | 542 | |
| 1155 | b | AGCCCCGTGTAGCCTCCGACGAGCTCTGGCAACGGCGCTGGCAGCTTCCTTGAAACATT | 1096 | |
| 543 | y | ATGCTGGCTATGAGCAGGTTCACCATGAGACCTCTCTGACCACTGACACGCTATTGCTGT | 602 | |
| 1095 | b | ATGCTGGCTATGAGCAGGTTCACCATGAGACCTCTCTGACCACTGACACGCTATTGCTGT | 1036 | |
| 603 | y | GCGCCCCGTTGCTGCACCCATTGAACCTGCTGTCTTCGCACACGGCTTCGGGGTGGCGT | 662 | |
| 1035 | b | GCGCCCCGTTGCTGCACCCATTGAACCTGCTGTCTTCGCACACGGCTTCGGGGTGGCGC | 976 | |

RESULT 6

US-09-970-516-1

03-05-270-318-1
; Sequence 1, Application US/09970516

; Patent No. US20020099029A1

FACEID NO: 052002005
: GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: No. US20020099029A1artis AG

APPL#CANI: NO: 0820020039023A1A1C1S AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of

;; TITLE OF INVENTION: polynucleotides encoding sphingosine kinases

;; FILE REFERENCE: 4-31617

;; CURRENT APPLICATION NUMBER: US/09/970,516

;; CURRENT FILING DATE: 2001-10-04

;; NUMBER OF SEQ ID NOS: 6

;; SOFTWARE: PatentIn version 3.1

;; SEQ ID NO 1

;; LENGTH: 1155

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: (1)..(1155)

;; OTHER INFORMATION:

;; US-09-970-516-1

Query Match 70.3%; Score 1124.6; DB 9; Length 1155;
Best Local Similarity 98.3%; Pred. No. 8.6e-286;
Matches 1136; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

2y 176 ATGATCCAGCGGCGGCCCGCGGGCGTCTCCCGCGCCCTGCGCGTGTGTGTG 235
Db 1 ATGATCCAGCGGCGGCCCGCGGGCGTCTCCCGCGCCCTGCGCGTGTGTGTG 60
2y 236 CTGAACCCCGCGCGCGCAAGGCAAGGCTTTCAGCTCTTCCGAGTCACTGAGGCC 295
Db 61 CTGAACCCCGCGCGCGCAAGGCAAGGCTTTCAGCTCTTCCGAGTCACTGAGGCC 120
2y 296 CTTTGGCTGAGCTGAATCTCTTTCAGCTGATCTCAGTGGCGGCGGAACACGG 355
Db 121 CTTTGGCTGAGCTGAATCTCTTTCAGCTGATCTCAGTGGCGGCGGAACACGG 180
2y 356 CGGAGCTGCTGCGTGGAGAGCTGGGCGGCTGGGAGCTCTGTGTGTGTGTGA 415
Db 181 CGGAGCTGCTGCGTGGAGAGCTGGGCGGCTGGGAGCTCTGTGTGTGTGTGA 240
2y 416 GACGGCTGATGACAGAGTGTGTGAACGGCTCATGGAGCGGCTGACTGGAGACCGCC 475
Db 241 GACGGCTGATGACAGAGTGTGTGAACGGCTCATGGAGCGGCTGACTGGAGACCGCC 300
2y 476 ATCCAGAGCCCTGTGTAGCTCCAGAGGCTCTGGCAACGGCTGGCAGCTTCCCTTG 535
Db 301 ATCCAGAGCCCTGTGTAGCTCCAGAGGCTCTGGCAACGGCTGGCAGCTTCCCTTG 360
2y 536 AACCATTTGCTGGCTATGAGAGGTCACCAATGAAGACTCTGTACCAACTGCACTA 595
Db 361 AACCATTTGCTGGCTATGAGAGGTCACCAATGAAGACTCTGTACCAACTGCACTA 420
2y 596 TTGCTGTGCGCGCGGCTGTGTACCATGAACCTGTCTGTGACAGCGCTTCCGGG 655
Db 421 TTGCTGTGCGCGCGGCTGTGTACCATGAACCTGTCTGTGACAGCGCTTCCGGG 480
2y 656 CTGCGCTCGTCTGTGTCTGAGCTGAGCTGGGCTTCAATGCTGATGAGCTTAGAG 715
Db 481 CTGCGCTCTTCTGTGTCTGAGCTGAGCTGGGCTTCAATGCTGATGAGCTTAGAG 540
2y 716 AGTGATTAAGTATCGGCTGTGGGGAGATGCGCTTCACTCTGGGCACTTCTGTGCTG 775
Db 541 AGTGATTAAGTATCGGCTGTGGGGAGATGCGCTTCACTCTGGGCACTTCTGTGCTG 600
2y 776 GCAGCCCTGGCACTACCGCGCGGCTGAGCTGCTCTCTAGGAAGTGGGTTTC 835
Db 601 GCAGCCCTGGCACTACCGCGCGGCTGAGCTGCTCTCTAGGAAGTGGGTTTC 560
2y 836 AAGACACTCTTCTCCCGTGTGGTCCAGAGGCGCGGTAGATGCAACCTGTGTGCA 895
Db 661 AAGACACTCTTCTCCCGTGTGGTCCAGAGGCGCGGTAGATGCAACCTGTGTGCA 720
2y 896 CTGAGAGCAGGTCCTTCTCACTGGCAGTGTGCGGACGAGACTTGTGTGTAGTC 955
Db 721 CTGAGAGCAGGTCCTTCTCACTGGCAGTGTGCGGACGAGACTTGTGTGTAGTC 780
2y 956 CTGCACTGTGCACTGCGACCTGGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1015

Db 781 CTGCACTGTGCACTGCACTGCACTGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Qy 1016 GCAGTGGCGCTGATGATCTGTTCTACGTGCGGCGGAGTGTGTGTGTGTGTGTGTGT 1075
Db 841 GCAGTGGCGCTGATGATCTGTTCTACGTGCGGCGGAGTGTGTGTGTGTGTGTGTGT 900
Qy 1076 CGCTCTCTCTGCGCATGAGAGGCGAGGCATATGAGTATGATGATGATGATGATGAT 1135
Db 901 CGCTCTCTCTGCGCATGAGAGGCGAGGCATATGAGTATGATGATGATGATGATGAT 960
Qy 1136 TATGTGCGCGTGTGTGCGCTTCCGCTTGGAGCCCAAGAGTGGGAAAGTGTGTGTGTGT 1195
Db 961 TATGTGCGCGTGTGTGCGCTTCCGCTTGGAGCCCAAGAGTGGGAAAGTGTGTGTGT 1020
Qy 1196 GATGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1255
Db 1021 GATGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Qy 1256 ATGCTCAGCGCTTGT 1315
Db 1081 ATGCTCAGCGCTTGT 1140
Qy 1316 GAAGAGCCCTTATGA 1330
Db 1141 GAAGAGCCCTTATGA 1155

RESULT 7

US-10-348-052-22

;; Sequence 22, Application US/10348052

;; Publication No. US20030219782A1

;; GENERAL INFORMATION:

;; APPLICANT: Saba, Julie D.

;; APPLICANT: First, Henrik

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION

;; TITLE OF INVENTION: OF SPHINGOLIPID METABOLISM AND/OR SIGNALING

;; FILE REFERENCE: 200116.405

;; CURRENT APPLICATION NUMBER: US/10/348,052

;; CURRENT FILING DATE: 2003-01-17

;; NUMBER OF SEQ ID NOS: 29

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 22

;; LENGTH: 1152

;; TYPE: DNA

;; ORGANISM: Homo sapiens

US-10-348-052-22

Query Match 70.0%; Score 1120; DB 15; Length 1152;

Best Local Similarity 98.3%; Pred. No. 1.4e-284;

Matches 1132; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 176 ATGATCCAGCGGCGGCCCGCGGGCGTGTCTCCGCGGCCCTGCCGCGTGTGTGTGT 235
Db 1 ATGATCCAGCGGCGGCCCGCGGGCGTGTCTCCGCGGCCCTGCCGCGTGTGTGTGT 60
Qy 236 CTGAACCCCGCGCGCGCAAGGCGCTTTCAGCTCTTCCGAGTCACTGAGCTGAGCGCC 295
Db 61 CTGAACCCCGCGCGCGCAAGGCGCTTTCAGCTCTTCCGAGTCACTGAGCTGAGCGCC 120
Qy 296 CTTTGGCTGAGGCTGAATCTCTTCACTGATGCTGATGCTGATGCTGATGCTGATGCTG 355
Db 121 CTTTGGCTGAGGCTGAATCTCTTCACTGATGCTGATGCTGATGCTGATGCTGATGCT 180
Qy 356 CGGAGCTGT 415
Db 181 CGGAGCTGT 240
Qy 416 GACGGCTGATGACAGAGTGTGTGAACGGCTCATGAGCGGCTGACTGGGAGACCGCC 475
Db 241 GACGGCTGATGACAGAGTGTGTGAACGGCTCATGAGCGGCTGACTGGGAGACCGCC 300
Qy 476 ATCCAGAGCCCTGTGTAGCTCCAGAGGCTCTGGCAACGGCTGGCAGCTTCCCTTG 535

1018 GATGAGGCGCTGATGTATGTGAAGTGTGTCAGGGCCCAAGTGCACCCAACTACCTTTGG 1077
1256 ATGGTCAGCGGTGGGTGGAGCCCGCCGACAGTGGAAAGCCCGCCAGCAGATGCCACCGCCA 1315
1078 ATGGTCTGTGGCAGCAGAGATGCCCCCATCCGCGCGGACTCCCGCGGGGCCACCTCCA 1137
1316 GAAGAGCCCTTA 1327
1138 GAAGAACCATAA 1149

RESULT 10
US-09-954-456-1756/c
Sequence 1756, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1756
LENGTH: 394
TYPE: DNA
ORGANISM: Homo sapiens

US-09-954-456-1756
Query Match 23.9%; Score 382.6; DB 9; Length 394;
Best Local Similarity 99.0%; Pred. No. 8.9e-91;
Matches 385; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1211 GTTAGGAGCGCGTCAGGGCCAGGTGCACCCAACTACTTCTGGATGCTGAGCGTTGC 1270
394 GTTAGGAGCGCGTCAGGGCCAGGTGCACCCAACTACTTCTGGATGCTGAGCGTTGC 335
1271 GTGAGAGCCCGCCAGCTGGAGGCCCGCCAGCAGATGCCACCGCCAGAGAGCCCTTATGA 1330
334 GTGAGAGCCCGCCAGCTGGAGGCCCGCCAGCAGATGCCACCGCCAGAGAGCCCTTATGA 275
1331 CCCCTGGGCGCGCTGTGCTTGTGTCTACTTGAGGACCCCTTCCCTCCCTAGGGC 1390
274 CCCCTGGGCGCGCTGTGCTTGTGTCTACTTGAGGACCCCTTCCCTCCCTAGGGC 215
1391 TCAGGGGCTGTCCACAGCTCTGTGGGGTGGAGAGACTCTCTGAGAGGGTGAGA 1450
214 TCAGGGGCTGTCCACAGCTCTGTGGGGTGGAGAGACTCTCTGAGAGGGTGAGA 155
1451 AGGTGGAGGCTATGCTTTTGGGGGGGACAGCCAGATGAAGTCTGGGTGAGGAGCCGAGC 1510

Db 154 AGTGGAGGCTATGCTTTGGGGGACAGCCACAATGAAGTCTGGGTGAGGAGCCAGC 95
Cy 1511 TGCGTGGGCCCACTGCTATGTATGAGGCTTCTAGTTTGTGTGAGACCCCGCCACG 1570
Db 94 TGGTGGGCCCACTGCTATGTATGAGGCTTCTAGTTTGTGTGAGACCCCGCCACG 35
Cy 1571 AACCAATCCAAATAAAGTGACATTCCCA 1599
Db 34 ACCAAATCCAAATAAAGTGACATTCCCA 6

RESULT 11
US-09-783-590-9248
Sequence 9248, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9248
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc feature
LOCATION: (68)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (193)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (220)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (221)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (236)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (289)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (297)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (302)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (322)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (337)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (350)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (356)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (367)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (382)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (384)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (386)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (391)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (400)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (412)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (451)
OTHER INFORMATION: n equals a.t.g, or c
US-09-783-590-9248

Query Match 17.9%; Score 286.6; DB 9; Length 480;
Best Local Similarity 84.4%; Pred. No. 1.6e-65;
Matches 391; Conservative 0; Mismatches 64; Indels 8; Gaps 7;

QY 312 AATCTCTTCAAGTATGCTCACTAGCGGGGAAACCAACGCGGGAGCTGGTGGGT 371
DB 10 AATCTCTTCAAGTATGCTCACTAGCGGGGAAACCAACGCGGGAGCTGGTGGGT 69
QY 372 CGAGGAGCTGGGCGCTGGGAGCTCTGTGTCTATCTGTGAGACGGGCTGATGCAAG 431
DB 70 CGAGGAGCTGGGCGCTGGGAGCTCTGTGTCTATCTGTGAGACGGGCTGATGCAAG 129
QY 432 AG-GTGTGAACGGGC-TCATGAGCGGGCTGACTGGG-AGACCGGCATCCAGAACCC 488
DB 130 AGAGTGGTGAACGGGCTTCATGAGCGGGCTGACTGGGAGACCGGCATCCAGAACCC 189
QY 489 TGTGTAGCTCCAGAGGCTCTGGCAACGGCTGACCTTGTGACCTTGTGACCTTGTG 548
DB 190 TGTGTAGCTCCAGAGGCTCTGGCAACGGCTGACCTTGTGACCTTGTGACCTTGTG 249
QY 549 GCTATG-AGCAGGTACCAATG-AAGACCTCTGACCACTGACGCTTATGCTGCGG 606
DB 250 GTTATGAAGCAGGTACCAATGAAGACCTCTGACCAATGACGCTTATGCTGCGG 309
QY 607 CCGGTGTCT--GTACCCATGAACCTGTCTGTCTGTGACACGCTTGGGGGTGCGCTCG 664
DB 310 GCCGGTGTGTGAACCATGGAACCTGTGTCTTGTGCAAAAGGTTTGGGGGTGCGG 369
QY 665 TTCTCTGT-GCTCAGCTGGCTGGGCTTCACTGTGATGTGACCTAGAGAGTGATAA 723
DB 370 TTCTTGTGTTTANCTGAGCTTGGGTTTNAATGTGATTTGAGACCGGAGTTAGAA 429
QY 724 GTATCGGCTGTGGGGAGATGCGCTTCACTTGGGACCTTC 766
DB 430 GTATCGGCTTGGGGAGATGCTTCACTTGGGACCTTC 472

RESULT 12
US-09-970-516-3
Sequence 3, Application US/09970516
Patent No. US2002009029A1
GENERAL INFORMATION:
APPLICANT: No. US2002009029A1; Applicant's AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REFERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04

NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1857
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1857)
OTHER INFORMATION:
US-09-970-516-3

Query Match 16.1%; Score 258; DB 9; Length 1857;
Best Local Similarity 63.3%; Pred. No. 6.3e-58;
Matches 396; Conservative 0; Mismatches 220; Indels 0; Gaps 0;
QY 193 CCCCGGGGGTGTCTCCCGGGGCTTCCCGGGGCTTCCCGGGTCTGGTCTGTGAAACCGCGCGCGG 252
DB 408 CACCCCTGACCTGCTACCTCGGCGCGGCTTCTTCTTATGCTCAATCCCTTTGGGGG 467
QY 253 CAAGGCAAGGCTTGGAGCTTCCCGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 312
DB 468 TCGGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 527
QY 313 AATCTCTTCAAGTATGCTCACTAGCGGGGAAACCAACGCGGGAGCTGGTGGGTCT 372
DB 528 GCTGTCTTCAACCTCATCCAGACAGAAACCAACGCGCGGGAGCTGGTCCAGGG 587
QY 373 CGAGGAGCTGGGCGCTGGGAGCTCTGTGTCTATCTGTGAGACGGGCTGATGCAAG 432
DB 588 GCTGAGCTGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGG 647
QY 433 GGTGTGAACGGGCTCATGAGCGGCTGACTGGGAGCGGCTGACTGGGAGCGGCTTCCAGAGCCCTGTG 492
DB 648 GGTGTGAACGGGCTCATGAGCGGCTGACTGGGAGCGGCTGACTGGGAGCGGCTTCCAGAGCCCTGTG 707
QY 493 TAGGCTCCAGAGGCTCTGGCAACGGCTGGGAGCTTCTGTGAGACCTTATGCTGCTGCTA 552
DB 708 CATCTCCCTTGGCGCTCGGGCAACGGGCTGGGAGCGGCTGGGAGCGGCTTCCAGAGCCCTGTG 767
QY 553 TGAGCAGCTACCAATGAAGACCTCTGACCACTGACGCTTATGCTGTGCGGCGCGGCT 612
DB 768 TGAGCAGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGG 827
QY 613 GCTGTACCCATGAACCTGTGTCTGTGCAACGCTTGGGAGCGGCTGGGAGCGGCTGGTCTGTCTGT 672
DB 828 TGGCACCCACTGAGCTGTCTCCGTGACGCTGGGCTTGGGAGCGGCTTGGGAGCGGCTTGGGAGCGG 887
QY 673 GCTCAGCTTGGCTGGGCTTCACTTGTGATGTGAGCTTAGAGAGTGAAGTATGCGG 732
DB 888 CCTGTGTGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGG 947
QY 733 TCTGGGGAGATGCGCTTCACTTGGGAGCTTCTGCTGTGAGCTTGGGAGCTTGGGAGCTTGGGAGCTT 792
DB 948 CTGGGAGCTGCGGCTTCACTTGGGAGCTTGGGAGCTTGGGAGCTTGGGAGCTTGGGAGCTTGGGAGCT 1007
QY 793 CGCGGGCGAGCTGGCTTACCTCCCTG 818
DB 1008 CGCGGGCGAGCTTCTCTTACCTCCCG 1033

RESULT 13
US-09-817-676A-13
Sequence 13, Application US/09817676A
Patent No. US20020042101A1
GENERAL INFORMATION:
APPLICANT: Spiegler, Sarah
APPLICANT: Kohama, Takatumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2001-03-26

| | | | |
|---|------|--|------|
| y | 613 | GCTGTCAACCCATGAACCTGCTCTCTGCACACGGCTTCGGGGCTCGCCTCGTTCCTGT | 672 |
| b | 834 | TGGCCACCACACTGGACCTGCTCTCGGTGAGCGTGCGCCTCGGGCTCCCGCTCTTTCTCCTT | 893 |
| y | 673 | GCTCAGCCTGGCCTGGGGGTTTCATTGCTGATGTGGACCTAGAGAGTGAATAAGTATCGGCG | 732 |
| b | 894 | CCTGTCTGTGGCCTGGGGCTTCGTGTCAAGATGTGATATCCAGACGAGCGCTTCAGGGC | 953 |
| y | 733 | TCTGGGGGAGATGCGCTTCACCTGTGGGACCTTCCTGCTGTGGCAGCGCTGCGCACCTA | 792 |
| b | 954 | CTTGGGCAGTGCCCGTTTACACTGSGCACGGTGTGGGCTTCGCCACACTGCACACCTA | 1013 |
| y | 793 | CCGGGCCCGACTCGGCTACCTTCCTG | 818 |
| b | 1014 | CCGGCAGCGCTCTCTACCTCCCCG | 1039 |

RESULT 14

Qy 21 LeuAsnProArgGlyGlyGlyGlyGlyAlaLeuGlnLeuPheArgSerHisValGlnPro 40
Db 61 CTGAACCGCGCGCGCGCAAGGCAAGGCTTTCAGCTCTTCGGAGTCACTGCGAGCC 120
Qy 41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgGlnHisAla 60
Db 121 CTTTGGCTGAGGCTGAATCTCTTCAGCTGATGCTCACTGAGCGCGGAGAACACGCG 180
Qy 61 ArgGluLeuValArgSerGluGluLeuGlyArgTirPaspAlaLeuValMetSerGly 80
Db 181 CGGAGCTGGTGGCTCGGAGGAGCTGGGCGCTGGAGCGCTCTGGTGGTCACTGTGA 240
Qy 81 AspGlyLeuMetHisGluValValAlaGlyLeuMetGluArgProAspTrpGluThrAla 100
Db 241 GAGCGGTGATGACAGGAGGTGACAGGCTCATGGAGCGGCTGACTGGAGACCGCC 300
Qy 101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLeu 120
Db 301 ATCCAGAAGCCCTGTGTAGCTCCAGCAGGCTCTGGCAACGCGCTGCAGCTTCCTTG 360
Qy 121 AsnHisThrAlaGlyTyrGluGlnValThrAsnGluAspLeuThrAsnCysThrLeu 140
Db 361 AACCATATCTGGCTATGAGCAGGTCAACATGAAGACCTCTGACCAACTGCACGTTA 420
Qy 141 LeuLeuCysArgProValLeuSerProMetAsnLeuSerLeuHisThrAlaSerGly 160
Db 421 TTGCTGTGGCGCGCGCTGTGTCTCACCATGAACCTGTCTCTGCACACGCTTCGGGG 480
Qy 161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
Db 481 CTGGCGCTCTCTCTGTCTGCTCAGCCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
Db 541 AGTGGAAGATATCGGCTCTGGGGAGATGCGCTTCACTCTGGGACCTCTCTGCTGTG 600
Qy 201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
Db 601 GCAGCCCTGGCACCTACCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 221 LysThrProLysProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240
Db 661 AAGACACCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Qy 241 LeuGluGlnValProSerHisTrpGlnValProAspGluAspPheValLeuVal 260
Db 721 CTGGAGGAGCCAGTGCCTCTCTCTGACAGTGTGCTGCGGAGGAGCTTGTGCTAGTC 780
Qy 261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaProMetGlyArgCys 280
Db 781 CTGGCAGTGTGCACTGCACCTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
Db 841 GCAGTGGCGTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
Db 901 CGGCTCTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Qy 321 TyrValProValAlaPheArgLeuGluProLysAspGlyValPheAlaVal 340
Db 961 TATGTGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Qy 341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360
Db 1021 GATGGGAATTGATGTTAGCGAGGCGTGCAGGCGGAGTGCACCAAACTACTTCTCG 1080
Qy 361 MetValSerGlyCysValGluProProProSerTrpLysProGlnMetProProPro 380
Db 1081 ATGTCACGCGTGTGCTGGAGCGCCCGCCAGCTGGAGAGCCCGCAGCAGATGCCACGCCA 1140

Qy 381 GluGluProLeu 384
Db 1141 GAAGAGCCCTTA 1152
RESULT 2
US-09-205-258-90
; Sequence 90, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
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; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
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; EARLIER APPLICATION NUMBER: 60/048,893
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; EARLIER APPLICATION NUMBER: 60/048,900
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; EARLIER APPLICATION NUMBER: 60/048,901
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; EARLIER APPLICATION NUMBER: 60/048,892
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; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974

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 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,897
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,898
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,962
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,963
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,877
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,878
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/070,923
 EARLIER FILING DATE: 1997-12-18
 EARLIER APPLICATION NUMBER: 60/092,921
 EARLIER FILING DATE: 1998-07-15
 EARLIER APPLICATION NUMBER: 60/094,657
 EARLIER FILING DATE: 1998-07-30
 NUMBER OF SEQ ID NOS: 1227
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 90
 LENGTH: 1533
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (12)
 OTHER INFORMATION: n equals a,t,g, or c
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (123)
 OTHER INFORMATION: n equals a,t,g, or c
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (1522)
 OTHER INFORMATION: n equals a,t,g, or c
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (1527)
 OTHER INFORMATION: n equals a,t,g, or c
 S-09-205-258-90

Alignment Scores:
 red. No.: 2,896-214 Length: 1533
 core: 1927.00 Matches: 371
 percent Similarity: 96.88% Conservative: 2
 est Local Similarity: 96.36% Mismatches: 11
 user Match: 95.63% Indels: 1
 B: 4 Gaps: 0
 S-09-784-810C-2 (1-384) x US-09-205-258-90 (1-1533)
 Y 1 MetAspProAlaGlyValLeuProArgProCysArgValLeuValLeu 20
 b 73 ATGGATCCAGCGGGCGGGCGGGCGGCTGCTCCGCGCGCCCTCGCTGCTGCTG 132
 Y 21 LeuAsnProArgGlyGlyLysGlyAlaLeuGlnLeuPheArgSerHisValGlnPro 40
 b 133 CTGAACCGCGCGCGCGGAGGGGAGGCGCTTGCAGCTCTCCGAGTCACTGCGACGCC 192
 Y 41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgAsnHisAla 60
 b 193 CTTTGGTGGCTGAGGCTGAATCTCCCTTACGCTGATGCTCACTGAGCGCGGAAACACGG 252
 Y 61 ArgGluLeuValAcgSerGluGluLeuGlyArgTrpAspAlaLeuValMetSerGly 80
 b 253 CGGAGCTGGTGGCTCGAGAGAGCTGGCGCGCTGGRACGCTCTGGTGGTCACTGTTGGA 312
 Y 81 AspGlyLeuMetHisGluValValAsnGlyLeu-MetGluArgProAspTrpGluThrAl 100

Db 313 GACGGCTGATGCACGAGGTGGTGAACGGGCTTCATGGAGCGGCTGACTGGAGACCGC 372
 Qy 100 alleGlnLysProLeuCySerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLe 120
 Db 373 CATCCAGAAAGCCCTCTGTAGCTCCAGCAGGCTCTGCAACGCGCTGGCAGCTTCCTT 432
 Qy 120 uAsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCyThrLe 140
 Db 433 RAACCAATTAATGCTGGCTATAGCAGGTCAACCAATGAAGACCTCCTGACACAGCT 492
 Qy 140 uLeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerG 160
 Db 493 ATTGCTGTGCGCGGCTGCTGTCAACCATGAACCTGTCTCTGACACAGCTTCGGG 352
 Qy 160 YLeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeu 180
 Db 553 GCTGCGCTCTTCTCTGTGCTCAGCTGCGCTGGGCTTCATGTGTGATGTGACCTAGA 612
 Qy 180 uSerAspLysTyrArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLe 200
 Db 613 GAGTGAGAAGTATCGGCGTCTGGGGAGATGGCTTCACTCTGGGCACCTTCTTGGCTCT 672
 Qy 200 uAlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPh 220
 Db 673 GGCAGCCCTGCGCACCTACCGCGCGCTGACCTCCCTGTAGGAAGAGTGGGTTTC 732
 Qy 220 eLysThrProAlaSerProValValGlnGlnGlyProValAspAlaHisLeuValPr 240
 Db 733 CAAGACACCTGCTCCCGCTGTGTGTCAGGAGGCGCGGTAGATGCACACCTTGTGCC 792
 Qy 240 oLeuGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVa 260
 Db 793 ACTGGAGGAGCCAGTGCCTCTCACTGGACAGTGTGTGCCGCGCAGGACTTTGTGTAGT 852
 Qy 260 lLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCy 280
 Db 853 CCTGGCACTGCTGCACCTCGACCTGGGCGAGTGAGATGTTTGTGCACCATGGCGCGCTG 912
 Qy 280 sAlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeu 300
 Db 913 TGCAGCTGGCGTCATGCACTCTTCTACGTGGCGGGGAGTGTCTCGTGCATGCTGCT 972
 Qy 300 uArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCyProTyrLeuVa 320
 Db 973 GCGCTCTTCTCGCCCATGGAGAGGCGAGGATATGGAGTATGAATGCCCTACTTGT 1032
 Qy 320 lTyrValProValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVa 340
 Db 1033 ATATGTGCCGCTGGTGGCTTCCGCTTGGAGGCCCAAGGATGGAAAGGTGTGTTGCACT 1092
 Qy 340 lAspGlyGluLeuMetValSerGluAlaValGlnGlnValHisProAsnTyrPheTr 360
 Db 1093 GGATGGGAATGATGTTAGCGAGCGCTGAGGCGCCAGGTCACCCCAAACTACTTCTG 1152
 Qy 360 pMetValSerGlyCyValGluProProSerTrpLysProGlnGlnMetProProPr 380
 Db 1153 GATGGTCACGGTGGGTGGAGCCCCCGCCAGCTGGAAGACCCAGCAGATGCCACCGCC 1212
 Qy 380 oGluGluProLeu 384
 Db 1213 AGAAGAGCCCTTA 1225
 RESULT 3
 US-09-970-516-5
 ; Sequence 5, Application US/09970516
 ; Patent No. 6610534
 ; GENERAL INFORMATION:
 ; APPLICANT: No. 6610534artis AG
 ; TITLE OF INVENTION: Induction of blood vessel formation through administration of
 ; TITLE OF INVENTION: polynucleotides encoding springosine kinases
 ; FILE REFERENCE: 4-31617
 ; CURRENT APPLICATION NUMBER: US/09/970,516
 ; CURRENT FILING DATE: 2001-10-04

NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 1149
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1149)
OTHER INFORMATION:
US-09-970-516-5

Alignment Scores:

Pred. No.: 61e-175 Length: 1149
Score: 1587.50 Matches: 302
Percent Similarity: 87.99% Conservative: 35
Best Local Similarity: 78.85% Mismatches: 45
Query Match: 78.78% Indels: 1
DB: 4 Gaps: 1

US-09-784-810C-2 (1-384) x US-09-970-516-5 (1-1149)

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DB 1 ATGACACAGTAGAATGCTCGAGGACTGCTCCACGGCCATGCGAGCTGCTGGTGTG 60
QY 21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
DB 61 CTGAACCCCGAGGGTGGCAAGGCAAGGCTCTGCAGCTCTTCAGAGCCGTGTGCAGCCC 120
QY 41 LeuLeuAlaGluAlaGluLeuSerPheThrLeuMetLeuThrGluArgAsnHisAla 60
DB 121 TTCCTGGAGGAGGAGAGAGTAACTTTAACTGATACTACCGACGAGGAGAACCATGTC 180
QY 61 ArgGluLeuValArgSerGluLeuGlyArgTrpAspAlaLeuValMetSerGly 80
DB 181 AGGAGCTGGTGTGTCAGAGGAGTGTGGTCACTGGAGCGCCCTGGCAGTCATGTCGGT 240
QY 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
DB 241 GATGGTCTGATGATGAGTGGTGAATGGCTAATGGAACGGCCGCTGGAGAGCTGCC 300
QY 101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLeu 120
DB 301 ATCCAGAAACCCCTGTGTAGCTCCCTCGAGGGCTCCGCAATGCGTGGCAGCTTCTGTG 360
QY 121 AsnHisTyraGlyTyraGluGlnValThrAsnGluAspLeuThrAsnCysThrLeu 140
DB 361 AACCATATCTGGTACGAGCAGGTGACTAATGAAGACCTGTCTCACTCACTGCACATG 420
QY 141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
DB 421 CTGTTGTGCGCGCGGCGCTGTCAACCATGAACCTGTCTCTCCCTGCACACTGCTTCTGGG 480
QY 161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
DB 481 CTGCGGCTCTATTCTGTGCTCAGTCTGCTGGGGCTTTGCTGCTGAGTGGACCTCGAG 540
QY 181 SerAspLysTyraArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
DB 541 AGTCAGAAGTACAGGCGCTTGGGGGAGATTCTGTTTTCACAGTGGGCACCTTCTTTCGCCA 600
QY 201 AlaAlaLeuArgThrTyraArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
DB 601 GCAAGCTTGGGATCTACCAAGGCGCACTGGCCCTACTCTCTCTGTAGAACTGTGGCCCT 660
QY 221 LysThrProAlaSerProValValGlnGlnGlyProValAspAlaHisLeuValPro 240
DB 661 AAGAGACCCGCTCT--ACACTGGTGCAGAGGCGCCGCTGCACACACACCTTGTCTCT 717
QY 241 LeuGluGlnValProSerHisTrpGlnValProAspGluAspPheValLeuVal 260
DB 718 CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 777

QY 261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
DB 778 CTGGTGTCTGTACACACCCACCTGAGTCCGAGCTGTTTCAGACACCATGGGCGCTGT 837
QY 281 AlaAlaGlyValMetHisLeuPheTyraValArgAlaGlyValSerArgAlaMetLeuLeu 300
DB 838 GAGGCTGGTGTATGATGCTGTTCTAGTACGTCGGGGGTGTCAAGGGCTGGCTGCTG 897
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DB 898 GCGCTCTTCTGGCCATGCAAGGCAAGCATATGGAACCTTGACTGTCCATACCTGGTT 957
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DB 958 CATGTGCGCGGTGGTGTGTTTCCGCTGGAGCCCGAGGAGGCGGTGTTTCTGTG 1017
QY 341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyraPheTrp 360
DB 1018 GATGAGGGCTGATGTTATGTGAAGCTGTGAGGCGCAAGTGCACCAAACTACCTTTGG 1077
QY 361 MetValSerGlyCysValGluProProSerTrpLysProGlnGlnMetProProPro 380
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QY 381 GluGluPro 383
DB 1138 GAAGAACCA 1146
RESULT 4
US-09-970-516-3
Sequence 3, Application US/09970516
Patent No. 6610534
GENERAL INFORMATION:
APPLICANT: No. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
FILE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REFERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 1857
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1857)
OTHER INFORMATION:
US-09-970-516-3
Alignment Scores:
Pred. No.: 1.7e-89 Length: 1857
Score: 856.50 Matches: 189
Percent Similarity: 51.43% Conservative: 63
Best Local Similarity: 38.57% Mismatches: 111
Query Match: 42.51% Indels: 127
DB: 4 Gaps: 6
US-09-784-810C-2 (1-384) x US-09-970-516-3 (1-1857)
QY 10 ValLeuProArgProCysArgValLeuValLeuLeuAsnProArgGlyGlyLysGlyLys 29
DB 418 CTGTCTACCTCGCGCGCGCGCTGCTCTTCTATGTGTCAATCCCTTTGGGGGTGGGGGCTG 477
QY 30 AlaLeuGlnLeuPheArgSerHisValGlnProLeuLeuAlaGluAlaGluLeuSerPhe 49
DB 478 GCGTGGCAGTGGTGTAAAGAACCACTGCTTCCCATGATCTCTGAAGCTGGGCTGCTCTTC 537
QY 50 ThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeu 69
DB 538 AACCTCATCCAGACAGAACCGACACACCGCGGAGGCTGGTCCAGGGGCTGAGGCTG 597

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2Y 70 GlyArgTyrPaspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAen 89
2b 598 AFTGAGTGGGATGGCATGCTACGGTCTCGGAGACGGGCTCTCCATGAGTGTGAAC 657
2Y 90 GlyLeuMetGluArgProAspTyrGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
2b 658 GGGCTCTAGATCGCCTGACTGGGAGGAGCTGTGAAGATCCCTGTGGGATCTCTCC 717
2Y 110 AlaGlySerGlyAsnAlaLeuAlaLeuAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
2b 718 TCGGGCTCGGCAACGGCTGGCGGAGAGTGAACACGACGGGGATTTGAGCGACGCC 777
2Y 130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
2b 778 CTGGGCTCGACTGTGTCTCACTGCTCAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 837
2Y 150 MetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSerLeu 169
2b 838 CTGGACCTGCTCTCGGTGAGCTGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 897
2Y 170 AlaTyrGlyPheIleAlaAspValAspLeuGluSerAspLysTyrArgArgGlyGlu 189
2b 898 GCGTGGGGCTTGTGTGATGTGATATCCAGAGCGAGCGCTTCAGGGCCCTTGGGCGAGT 957
2Y 190 MetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArgGlyArg 209
2b 958 GCCCGCTTCACACTGGGCAAGTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 1017
2Y 210 LeuAlaThrLeuProVal
2b 1018 CTCTCTACTCTCCCGCCACTGTGGAACCTGCTGCGCCACCCCTGCGCCATAGCCTGCT 1077
2Y 215
2b 1078 CTGGCAAGTCGAGTGAACCTAACCCAGACCCAGCCGCCGCCCATGGCCCATCACCC 1137
2Y 215
2b 1138 CTGCATCGTGTGTGTGTGACTGCTGTCTTCCCTGCGCCAGCCTGCGCTGCTCTCT 1197
2Y 215
2b 1198 GCGTCCAGAACCCCTGCCATCTGTCTCCCTCAACGGTGGGGGCCAGAGCTGGCTGG 1257
2Y 215
2b 1258 GACTGGGTGGGCTGGGATGCTCGCTGTCCCGGACCCACTGCTGTCTTCACCTCTCT 1317
2Y 216 -----GlyArgValGlyPheLysThrProAlaSer-----ProValValValGln 230
2b 1318 GCGCTCTCCCAAGGCAGCTCTACACTCACCCGTCTCCGAAGGGGCCCGGTAATCCGCCA 1377
2Y 231 Gln-----GlyPro 233
2b 1378 TCTCTGGGCTCCACTTCCACCTCCACCTGTATGTCGGGTAGGGGCTTCCACCTGGGCCCG 1437
2Y 234 ValAspAlaHisLeuValProLeuGluGlnValProSerHisTyrPheGlnValValPro 253
2b 1438 CCGGACCACTGCTGCTCGCTGGGACCCCGCTGCCAGACTGG---GTGACGCTG 1494
2Y 254 AspGluAspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPhe 273
2b 1495 GGGGGGATTTGTGTCTATGTGGCCATCTCGCCACGACCACTAGGCGGTGACTGTGTG 1554
2Y 274 AlaAlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGly 293
2b 1555 GCAGCTCCGCATCGCGCTTCGACGAGCGCTGTGTGACCTGTGTGGTGGGTAGCGGC 1614
2Y 294 ValSerArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMetGlu 313
2b 1615 ATCTCGGGGCTGCGTGTGTGGGCTTTCTTGTGGCCATGGAGCGGTGAGTACCTTCAGC 1674
```

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QY 314 TyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLysAsp 333
Db 1675 CTGGGCTGTCCGAGCTGGGTACGCGCGCGCCCGCTTCCCTTAGAGCGCTCACA 1734
QY 334 GlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGlyGln 353
Db 1735 CCACGGCGCTGTCTACAGTGGACGGGAGCAGGTGAGTATGGCCGCTACAGGCACAG 1794
QY 354 ValHisProAsnTyrPheTyrMetValSerGlyCysValGluProProProSerTrpLys 373
Db 1795 ATGACCCCTGGCATCGGTACACTGCTCACTGGG-----CCTCTGGCTGC--- 1839
QY 374 ProGlnGlnMetProProProGluGluPro 383
Db 1840 -----CCGGGGCGGAGCCC 1854

RESULT 5
US-09-620-312D-796
; Sequence 796, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radcoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: Pt_FL_genes version 1.0
; SEQ ID NO 796
; LENGTH: 2462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(1464)
; US-09-620-312D-796

Alignment Scores:
Pred. No.: 1,24e-12 Length: 2462
Score: 198.00 Matches: 92
Percent Similarity: 41.02% Conservative: 77
Best Local Similarity: 22.33% Mismatches: 160
Query Match: 9.83% Indels: 83
DB: 4 Gaps: 18

US-09-784-810C-2 (1-384) x US-09-620-312D-796 (1-2462)
QY 16 ArgValLeuValLeuLeuAsnProArgGlyGlyGlyAlaLeuGlnLeuPheArg 35
Db 379 AAGGCCACTGTTTCTCAATCTCGAGCTTGCAGAAAGAACCCAGGACTCTATTGAA 438
QY 36 SerHisValGlnProLeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGlu 55
```



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; OTHER INFORMATION: H37RV
US-09-103-840A-1

Alignment Scores:
Pred. No.: 46.2 Length: 4411529
Score: 126.50 Matches: 43
Percent Similarity: 43.54% Conservative: 21
Best Local Similarity: 29.25% Mismatches: 62
Query Match: 6.28% Indels: 21
DB: 3 Gaps: 4

US-09-784-810C-2 (1-384) x US-09-103-840A-1 (1-4411529)

QY 7 ProArgGlyValLeuProArgProCysargValLeuValLeuLeuAsn----- 22
Db 3594372 CCGGCCCGCATGTCACACGGCTAAGCCCATGCGCTCTCTCTCAACGGCGCAGCCGCG 3594431
QY 23 ProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisVal----- 38
Db 3594432 CCGGCATCGTCACACGGCCTAAGCTCGTGCCTCATGCGTGCAGTGTGATCGTCAACCC 3594491
QY 39 -----GlnProLeuLeuAla-----GluAlaGlu 46
Db 3594492 ACTGGACCGCCACACACACACCGCGCGCGACCTGCTGGCGCAGCCCTCGAAGACCGCG 3594551
QY 47 IleSerPheThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSer 66
Db 3594552 CTTACGTCACCGTTTGAGCACACCAACACCGCGGTCAACGGACCGAACTCGACAGGCG 3594611
QY 67 GluGluLeuGlyArgTrpAspAlaLeuValMetSerGlyAspGlyLeuMetHisGlu 86
Db 3594612 GCGGTAGCGACGCGGGTGACCTGTCGTGGTGCATGCGCGCGATGCGCAGGTAAAGCGCG 3594671
QY 87 ValValAsnGlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLysPro---Leu 105
Db 3594672 GTAGTACAGGCGATGCTGGGCGCGCCCGGCACGCGCGTCCGACCGGTGCACGCGGTT 3594731
QY 106 CysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAlaGly 125
Db 3594732 GCGGTGTGTCGCGCGCGTTCGCCAACGTACTAGTTCGCGCGCTAGGGATTCCGCGGAC 3594791
QY 126 TyrGluGlnValThrAsnGlu 132
Db 3594792 CCGATCGTGCACCAACCAA 3594812

RESULT 10
US-09-134-000C-211
; Sequence 211, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-211

Alignment Scores:
Pred. No.: 6.7e-05 Length: 894
Score: 125.50 Matches: 52
Percent Similarity: 41.89% Conservative: 41
Best Local Similarity: 23.42% Mismatches: 75
Query Match: 6.23% Indels: 54
DB: 4 Gaps: 10

```


JS-09-784-810C-2 (1-384) x US-09-134-000C-211 (1-894)

42 LeuAlaGluAlaGluSerPheThrLeuMetLeuThrGluArgAsnHisAlaArg 61
19 CTCAAGCAACAAGACTTAATATAGCGCTCTTACACTGATTACGCTGGACATGAAAAA 78
62 GluLeuValArg-----SerGluGluLeu----- 69
79 GAATTGACGAGGAAGACTTCAGAAACAACCTTACTCTCTGTCGAGACTTAGACGTT 138
70 GlyArgTrpAspAlaLeuValMetSerGlyAspGlyLeuMetHisGluValValAsn 89
139 TCAACTTTCCATCCTAGTCTGCTAGCGCGGATGGCACATACATAATGCTAAT 198
90 GlyLeuMetGluArgProAspTrpGluThrAlaLeuGlnLysProLeuCysSerLeuPro 109
199 TCATTAATT-----CCATATGATTCAATATT-----CCTTAAGCTATATTCCA 243
110 AlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
244 TCGGGCTCTGGAATGATTTTGCACGAGGGGTTGATATCAAGAAATATTGATAAGCA 303
130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
304 TTGCATCAAAATCCTGGCCACAGA-----CGACCA 333
150 MetAsnLeuLeuSerLeuHisThrAlaSer-----GlyLeuArgSer 163
334 AAGAAATTCAAACAATTCATTATGTAAAGCAACCAAGAAATCGCTTAGCCACC 393
164 PheSerVal-----LeuSerLeuAlaTrpGlyPheAlaAspValAspLeuGlu 180
394 AATAATGTTGGCTTAGGTTGGATGGCGCA-----ATCGTGGAAAAACCAACGAA 444
181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
445 TCGTCATCAAAAAAGCCCTTAAT-----AAATTTAAGCTTGGCTTCCTTATATT 498
201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
499 TCTTCA-----ATCATTCATGCTCTTTT 522
221 LysThrProAlaSerProValValValGlnGlnGlyProVal-AspAlaHisLeuValPr 240
523 AGACAAAAAGGCTTTCCAAATTTTAGTTGAATGAATGTTAAACAATACATTTAATCGT 582
240 oLeu 241
583 GCTT 586

RESULT 11
US-09-107-532A-3500
Sequence 3500, Application US/09107532A
Patent No. 6581275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
City: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GPC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3500:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...942
SEQUENCE DESCRIPTION: SEQ ID NO: 3500:
US-09-107-532A-3500

Alignment Scores:
Pred. No.: 0.000476 Length: 942
Score: 118.50 Matches: 53
Percent Similarity: 44.22% Conservative: 58
Best Local Similarity: 21.12% Mismatches: 89
Query Match: 5.88% Indels: 51
DB: 4 Gaps: 10

US-09-784-810C-2 (1-384) x US-09-107-532A-3500 (1-942)

QY 16 ArgValLeuValLeuLeuAsnProArgGlyGlyLysAlaLeuGlnLeuPheArg 35
DB 64 AAGTTTTATTAGTGTGTAACCCAGCTTACGGCGGTGACACAGCA-----AAG 111
QY 36 SerHisValGlnProLeuLeuAlaGluAlaGluIleSerPhe-----ThrLeuMet 52
DB 112 GAATTTGAGCAATTAGCGATAGCAAAATTCGAATCGGTGTTGATGAAGTGGTCTTG 171
QY 53 LeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArgTrp 72
DB 172 CATACAAAAAAGCAGGGGATGCAGAAAACTTTACTCGCGAAGCGGTACGGAAGGTAT 231
QY 73 AspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsnGlyLeuMet 92
DB 232 CATAGTGTGTTGTCATGGCGGAGATGGAACAGTCAACGAGGAATCAGTGAATCGCT 291
QY 93 Glu-----ArgProAspTrpGluThrAlaLeuGlnLysProLeuCysSerLeuPro 109
DB 292 GAACAGAACATCGGCCAAATTTCCGA-----TTTTTCCCA 327
QY 110 AlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
DB 328 TTGGTACGCTGATGACTTGGCTCGAGCATTAGGGATACCGCTAGACCTAGGAAGCG 387
QY 130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
DB 388 ATCAATCATTTTTCGATTGAATCA-----GTCAAGCCA 420
QY 150 MetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSerLeu 169
DB 421 TTGATATTGAAAAATAAATAGAC-----GACTATTTTATGAATGTCGTC 465

Qy 170 AlaTrpGlyPheIleAlaaspVal-----AspLeuGluSerAspIysTyrArgArgLeu 187
Db 466 GCATTCGGCTCTATCCCTGAATCAATCAATGATGATAGATCGGAGAGAAAGAGCAATTT 525
Qy 188 GlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArg 207
Db 526 GGAATACTAGCTTATTCATGTCAGGAATCAAAACAGTTAGCTTCCACACAATCTACTCG 585
Qy 208 GlyArgLeu-----AlaThrLeuProValGly 216
Db 586 TTCACGTAGAGTTGATGGAAGAAGAGAAATTCAGAGCAGTACCTTGTGTATAGGA 645
Qy 217 ArgVal-----GlyPheLysThrProAlaSerProValValGlnGlnGly 232
Db 646 CTAACCTAATCAGTCGCGGTTTGAACATTACTTCCAAATCCAAAGTGGATGATGT 705
Qy 233 ProValAspAlaHisLeuValProLeuGluGlu 243
Db 706 ARGCTC-----CATTTGGTTTATTTAAAGAT 732
RESULT 12
US-08-961-527-332/c
; Sequence 332, Application US/08961527
; Patent No. 8420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 35,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 332:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-332
Alignment Scores:
Pred. No.: 0.00193 Length: 900
Score: 113.00 Matches: 47
Percent Similarity: 49.39% Conservative: 34
Best Local Similarity: 28.66% Mismatches: 54
Query Match: 5.61% Indels: 29
DB: 4 Gaps: 8
US-09-784-810C-2 (1-384) x US-08-961-527-332 (1-900)
Qy 16 ArgValLeuValLeuAenProArgGlyGlyLysAlaLeuGlnLeuPheArg 35

Db 472 AAAGCAATGTAATATCAACCTACTCTCTGGTGGCAGAGGCTTTG----- 425
Qy 36 SerHisValGlnProLeuLeuAlaGluAlaGluSerPheThrLeuMet----- 52
Db 424 GATTACAAAGAAAGCTGGAGATAAAGCAAAAGATACTTTGAATATGTTGAACCAAA 365
Qy 53 LeuThrGluArgGAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArgTip 72
Db 364 ATTACCGMAAAGCGCTGGATGCAACATTTCTGTAAGAGCTTCTCGTGACGATAT 305
Qy 73 AspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsnGlyLeuMet 92
Db 304 GATCAGTGGTGTGTGTTGGTGGAGATGGAATCTCAATGAAGTCATTTCAGGTATTGAT 245
Qy 93 GluArgProAspTTPGluThrAlaIleGlnIysProLeuCysSerLeuProAlaGlySer 112
Db 244 GAGAGA---GACTAC-----ATTCTTAAG---TTAGGATTATCCCGGCGGTACG 200
Qy 113 GlyAsnAlaLeuAlaLaserLeuAsnHisTyrAlaGlyTyrGluGlnValThrAsnGlu 132
Db 199 GGTAACCTCATTCACAAACTTTTGGAA-----ATCAATCAA 164
Qy 133 Aspleu-----LeuThrAsnCysThrLeu-----LeuLeuCysAr 144
Db 163 GACATCGATGCGCAATGAGAACTGGATTGATTAAACCAATAGATTGATCGGT 104
Qy 144 gProValLeuSerProMetAenLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPh 164
Db 103 AAAGCAATGACAACACTATTGTTGGTTATATCTTTAGTATCGTCTCTGCGTGGCGGATT 44
Qy 164 eSerValLeu 167
Db 43 CACAATGTTG 34
RESULT 13
US-09-134-000C-408
; Sequence 408, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 408
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-408
Alignment Scores:
Pred. No.: 0.00242 Length: 1035
Score: 113.00 Matches: 71
Percent Similarity: 33.14% Conservative: 45
Best Local Similarity: 20.29% Mismatches: 132
Query Match: 5.61% Indels: 102
DB: 4 Gaps: 13
US-09-784-810C-2 (1-384) x US-09-134-000C-408 (1-1035)
Qy 19 ValLeuLeuAenProArgGlyGlyLysAlaLeuGlnLeuPheArgSerHisVal 38
Db 34 GTGATTATATAATCCAAACGTCAGGAAAA-----GAGTTAATCAAAAGAACTTA 81
Qy 39 GlnProLeuLeuAla-----GluAlaGluIleSerPheThrLeu 51
Db 82 GCCGATATTTTATCTATTATTTTAAAGATGTGGTTATGAAGCCAGTCGATTTGCCGACC--- 138

2y 52 MetLeuThrCluArgArgAsnHisAlaArgGluLeuValArgSerGluLeuLeuGlyArg 71
2b 139 -----ACACCAAGAAATTCAGCACCAATGAAGCACATCGTGCTCGCGGACAGA 192
2y 72 TrpAspAlaLeuValMetSerGlyAspGlyLeuMetHisGluValValAengly--- 90
2b 193 TTTGATTACTAGTACGCGTGGAGATGGACCAATTAAGTCTGTGATGGATT 252
2y 91 -----LeuMetGluArgProAspTrpGluThrAlaIleGlnIleProLeuCysSerLeu 108
2b 253 GTCCTGTTGAAGCGGCCCT-----AAATGGCTATTATT 288
2y 109 ProAlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyAlaGlyTyrGluGln 128
2b 289 CCGTCTGGAACGACGATGACTATGACCGGCGCTTGAAG----- 327
2y 129 ValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSer 148
2b 328 -----ATTCTCTGTGATAATATCGTTAAGGCACGACAGTGAATAA 369
2y 149 ProMetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSer 168
2b 370 AAAATCAAACTGTCAAAATGATATGGCCAGCGGCAAAATTAATTTCAATATT 429
2y 169 LeuAlaTrpGlyPheIleAlaAspValAspLeuGluSerAspIleTyArgArgLeuGly 188
2b 430 GCGCGGGTGGTCACTTAACGGAAGTCTTATGAAGTTCCG----- 471
2y 189 GluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaIleLeuArgThrTyrArgGly 208
2b 472 -----TCAAGTGTGAAGTATTTTGGT 495
2y 209 ArgLeuAlaThrLeuProValGly-----ArgValGlyPheIleThrPro 223
2b 496 TACTAGCTAGTACTACCAAGAGCGGAAATGTTGCCCGGAGTG----- 540
2y 224 AlaSerProValVal-----ValGlnGlnGlyProValAsp 235
2b 541 ----AGCCGATTAATGGCATGACGTATGATGAGGTGTGTACGAGGCAATCATCA 597
2y 236 AlaHisLeuValProLeuGluGlnValProSerHisTrpGlnValValProAspGlu 255
2b 598 ATGTTTTCCTAGGGTGACTAACTCGGTGGGTGTTTGAACAATCGTACCAT--- 654
2y 256 AspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAla 275
2b 654 ----- 654
2y 276 ProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyValArgAlaGlyValSer 295
2b 655 -----GCTAAATTAGACGATGTAAGTTTTCATTAATCATTTGTAATAACACGCCAATATT 708
2y 296 ArgAlaMetLeuLeuArgPheLeuAlaMetGluLyseGlyArgHisMetGluTyrGlu 315
2b 709 TTTGATTTCTTCATTAGTTAGTTCGTTAATGTTAATGTTGGAAGCATGTTGAACATCAT 768
2y 316 CysProTyLeuValTyrValProValValAlaPheArgLeuGlu-----ProIleAsp 333
2b 769 -----CGACTGATCTATACAAAGACGACGCTATTACATGTCAGAAACGTTAGAAAAGAAC 822
2y 334 GlyLyseGlyValPheAlaValAspGlyGlu 343
2b 823 AATAAATGATGATTAATTAGATGTGAA 852

RESULT 14

JS-09-221-017B-1064/c

Sequence 1064, Application US/09221017B

Patent No. 6444799

GENERAL INFORMATION:

APPLICANT: ROSS, Bruce C.

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USSES THEREOF

NUMBER OF SEQUENCES: 1120

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1064:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...1003
US-09-221-017B-1064

Alignment Scores:
Pred. No.: 0.00514 Length: 1003
Score: 110.00 Matches: 82
Percent Similarity: 35.26% Conservative: 58
Best Local Similarity: 20.65% Mismatches: 139
Query Match: 5.46% Indels: 118
DB: 4 Gaps: 19

US-09-784-810C-2 (1-384) x US-09-221-017B-1064 (1-1003)

Qy 16 ArgValLeuValLeuLeuAsnProArgGlyGlyGlyLysAlaLeuGlnLeuPheArg 35
Db 950 AAGATTCTAGCCATTATCAATNCCATATCGGGCATCGGATCG-----AAA 906
Qy 36 SerHisValGlnProLeuLeuAlaGlu-----AlaGluIleSerPheThrLeuMetLeu 53
Db 905 AGCAACATACCGAGCCTTATAGCGGATGATTCCGCCCATGCTCTCACGAACTCTTTATC 846
Qy 54 Thr-----GluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArg 71
Db 845 ACCTATTGCAACGTGCTGCGCCCATGCACTGGAATTGCGACGACCAAGCAGTGGAGAACAT 786

| | | | |
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| QY | 72 | TTPAspAlaLeuValValMetSerGlyAspGlyLeuMethHisGluValValAsnGlyLeu | 91 |
| DB | 785 | TACGACTCGGTCATTGCGTAGGAGGCGATGCAACGGTGAACGAGATACCCCAAGCCCT | 726 |
| QY | 92 | MetGluA+gProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuProAlaGly | 111 |
| DB | 725 | -----CGCTACACCGATGTAGTCTGGTATCTGTCGGAAGCA | 687 |
| QY | 112 | SerGlyAsnAlaLeuAlaAlaSerLeuAsn----- | 121 |
| DB | 686 | TCAGGCAACGGTGGCACGTGGCCCTCAAGCTGCCACTACCTCGGGAAGCTCTCGNA | 627 |
| QY | 122 | ----HisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu | 140 |
| DB | 626 | GTGATCAGAGCCGAGCATGTTCCGACC-----ATCAGTCTGTGTGAA | 585 |
| QY | 141 | LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly | 160 |
| DB | 584 | CGCGATAGTGGCCCTTTCTTTTGCACTGCGGATTG----- | 549 |
| QY | 161 | LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu | 180 |
| DB | 548 | -----GGATTGATCCGAGGTT----- | 531 |
| QY | 181 | SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu | 200 |
| DB | 530 | ACGAGAANTCGCCCAAGCGGTAGTCGA----- | 501 |
| QY | 201 | AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe | 220 |
| DB | 500 | -----GGCCTATCACTTAT | 486 |
| QY | 221 | LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHis----- | 237 |
| DB | 485 | GCGCAACCATGATCGAGAGTTACTCCAAAACGAACGAGGATCCAACTGACGATAG | 426 |
| QY | 238 | ----LeuValProLeuGlu-GluGlnValProSerHisTrpGlnValValProAspGluAs | 256 |
| DB | 425 | ACGGCAATCTCTTGAGGAGAAAGCTTCTCTCGTCAC-----TTGGTGCCA----- | 380 |
| QY | 256 | pPheValLeuValLeuAlaLeuLeuHisHisSerHisLeuAlaSerGluMetPheAlaAlaPr | 276 |
| DB | 379 | -----ATGCGCCCGAGTATGGCAATAACGCCTTATATCGTCC | 342 |
| QY | 276 | oMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGly----- | 293 |
| DB | 341 | ATTACGGATTTGGAGGATGTAAATGGATAGTTATTATTCGCTCTTCAATCCATT | 282 |
| QY | 294 | -ValSerArgAlaMetLeuLeuArgLeuPheLeu- --AlaMetGluLysGlyArgHisMe | 312 |
| DB | 281 | GGAACTCCACAATTTGGCTTTTACAACTCTTTACCAAGCGTATCAACAGCAACTCCAATCT | 222 |
| QY | 312 | tGlu--TyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluPr | 331 |
| DB | 221 | GGACACTTATAGCCCGGAACCTGATCAT-----GA | 189 |
| QY | 331 | oLysAspGlyLysGlyValPheAlaValAspGlyGlu-LeuMetValSerGluAlaValG | 351 |
| DB | 188 | GGGTGAGACAGAGGCGTAATGCACCTCGATGGCGATCTGTCTATGTCGTAAGCGCAT | 129 |
| QY | 351 | InGlyGlnVal-----HisProAsnTyrPheTrpMetValSerGlyCysValG | 367 |
| DB | 128 | TCGATATCGCACCTTAGCCCGGTCACTCAGAGTTATTG-----CTACTGAACCTCACACTTG | 72 |
| QY | 367 | luProProProSerTrp--LysProGlnGlnMetProProProGlu | 381 |
| DB | 71 | AAAGTCCCACTCTTTCTTAAATAACCAATAAAAATCCCGTAACCGGAG | 251 |

GENERAL INFORMATION:

```

APPLICANT: Charles Kunsch
           Gil H. Choi
           Patrick S. Dillon
           Craig A. Rosen
           Steven C. Barash
           Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 13542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 154:
US-08-956-171E-154

Alignment Scores:
Pred. No.: 0.584 Length: 13542
Score: 108.00 Matches: 70
Percent Similarity: 35.52% Conservative: 60
Best Local Similarity: 19.13% Mismatches: 126
Query Match: 5.36% Indels: 110
DB: 4 Gaps: 18

US-09-784-810C-2 (1-384) x US-08-956-171E-154 (1-13542)
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Db 5619 CQTGCTAGATCAATTATTAAACCCGACATCAGGTAAA-----GAGCTATTATAA 5572
QY 36 SerHisValGlnProLeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGlu 55
Db 5571 -----AGAAATTAACCTGATGCTTAAATAAATTAGAA 5539
QY 56 ArgATGAsnHisAlaArgGluLeuValArgSerGluGluLeuGly----- 70
Db 5538 AAAGCGGATATGAAACGAGTGATATGCAACCGAGAAATAAGTGATGCCACACTTGAA 5479
QY 71 -----ArgTrpAspAlaIleValValMetSerGlyAspGlyLeu 83
Db 5478 GCAGAAAAGAGTATGCATGAAATTTATGATGTTATTAATCGTCGAGGTGGTGAACA 5419
QY 84 MetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLys 103

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| 5418 | TTAAATGAAGTAGTAAATGCTATCGCAGAAAGCCCTAAAT | ProLeuSerLeuProAlaGlySerGlyAsnAlaLeuAlaAalaSerLeuAsnHisTyr | 123 |
| 5373 | AAGCTAGGTGTCATCTCTATGGGTACTGTTAATGACTTTGGACGTGCATTCGCAT | AAAGCTAGGTGTCATCTCTATGGGTACTGTTAATGACTTTGGACGTGCATTCGCAT | 5320 |
| 124 | AlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCys | AlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCys | 143 |
| 5319 | -----ATACCTAATGAC----- | -----ATACCTAATGAC----- | 5308 |
| 144 | ArgProValLeuSerProMetAsn-----LeuLeuSerLeuHisThrAlaSerGlyLeuArg | ArgProValLeuSerProMetAsn-----LeuLeuSerLeuHisThrAlaSerGlyLeuArg | 162 |
| 5307 | -----ATCATGGGGCAGCTGTGATGTCATCATTTGAAGGTCAITTCCTACTAAA----- | -----ATCATGGGGCAGCTGTGATGTCATCATTTGAAGGTCAITTCCTACTAAA----- | 5263 |
| 163 | SerPheSerValLeuSerLeuAlaThrGlyPheIleAlaaspValAspLeuGluSerAsp | SerPheSerValLeuSerLeuAlaThrGlyPheIleAlaaspValAspLeuGluSerAsp | 182 |
| 5262 | -----GTGATGATATTCGGTAAATGAATAAT | -----GTGATGATATTCGGTAAATGAATAAT | 5239 |
| 183 | LysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAla | LysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAla | 202 |
| 5238 | CGATAC-----TTTATTAAATTTAGCTGCA | CGATAC-----TTTATTAAATTTAGCTGCA | 5215 |
| 203 | LeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPheLysThr | LeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPheLysThr | 222 |
| 5214 | -----GGCGGCAATTTGACG-----CAAGTCTCTTATGAAACA | -----GGCGGCAATTTGACG-----CAAGTCTCTTATGAAACA | 5182 |
| 223 | ProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValProLeuGlu | ProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValProLeuGlu | 242 |
| 5181 | CCG---AGTAAATGGAATCTATTGTTGGTCCATTT---GCTATTACATCAAGGTTTC | CCG---AGTAAATGGAATCTATTGTTGGTCCATTT---GCTATTACATCAAGGTTTC | 5128 |
| 243 | GluGlnValProSer-----HisTrpGlnValVal | GluGlnValProSer-----HisTrpGlnValVal | 252 |
| 5127 | GAATGTTACCTCAAATGAAAGCTGTAGATTTAAGAAATTCGATATGATGATGTTTC | GAATGTTACCTCAAATGAAAGCTGTAGATTTAAGAAATTCGATATGATGATGTTTC | 5068 |
| 253 | ProAspGluAspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMet | ProAspGluAspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMet | 272 |
| 5067 | CAAGGAGNAGCATTAATTATCTTTTAGTTTAAACAAATTCATGGCAGGATTTGAAAA | CAAGGAGNAGCATTAATTATCTTTTAGTTTAAACAAATTCATGGCAGGATTTGAAAA | 5008 |
| 273 | PheAlaAlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAla | PheAlaAlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAla | 292 |
| 5007 | TTA---GTCCCGACGCTAAGTGTAGATGACGGCTATTTTACGTTAATATAGTTGAAAA | TTA---GTCCCGACGCTAAGTGTAGATGACGGCTATTTTACGTTAATATAGTTGAAAA | 4951 |
| 293 | GlyValSerArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMet | GlyValSerArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMet | 312 |
| 4950 | TCA---AACCTTGCAGAACTTGGTCATATATATGACTTTAGCTTCAGAGGAGNACATACT | TCA---AACCTTGCAGAACTTGGTCATATATATGACTTTAGCTTCAGAGGAGNACATACT | 4894 |
| 313 | GluTyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLys | GluTyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLys | 332 |
| 4893 | ARGCAT-----CCTAAAGTTATTATTTGAAAAAGCAAGCAATTAATATTTTCATCA--- | ARGCAT-----CCTAAAGTTATTATTTGAAAAAGCAAGCAATTAATATTTTCATCA--- | 4843 |
| 333 | AspGlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGly | AspGlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGly | 352 |
| 4842 | -----TTACAGACACTTACAACTAAATGTAGATGAGCAATATGTTGGT | -----TTACAGACACTTACAACTAAATGTAGATGAGCAATATGTTGGT | 4801 |
| 353 | GlnValHisProAsnTyr | GlnValHisProAsnTyr | 358 |
| 4800 | AAATTACCAGCAATTTTC | AAATTACCAGCAATTTTC | 4783 |

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search completed: February 27, 2004, 22:07:57
job time : 2740 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

M protein - nucleic search, using frame_plus_p2n model

Run on: February 27, 2004, 20:01:08 ; Search time 397 Seconds
(without alignments)
3489.338 Million cell updates/sec

Title: US-09-784-810C-2
Perfect score: 2015
Sequence: 1 MDPAGGPRGLPRPCRVLV.....CVERPPSKNQMPPEEPL 384

Scoring table: BLOSUM62

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|-------------|-------------|
| Xgapop 10.0 | Xgapext 0.5 |
| Ygapop 10.0 | Ygapext 0.5 |
| Fgapop 6.0 | Fgapext 7.0 |
| Delop 6.0 | Delext 7.0 |

Searched: 2353733 seqs, 1803733377 residues

Total number of hits satisfying chosen parameters: 4707466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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DB=Published Applications_NA -QPM=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62
TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
MAXLEN=2000000000 -USER=US09784810 @CGN 1 1 333 @runat_26022004_164546_3880
NCPU=6 -ICPU=3 -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| result No. | Score | Query Match | Length | ID | Description |
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|------------|-------|-------------|--------|----|-------------|

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|----|--------|-------|------|----|---------------------|-------------------|
| 1 | 2015 | 100.0 | 1600 | 9 | US-09-784-810A-1 | Sequence 1, Appli |
| 2 | 1962 | 97.4 | 1152 | 15 | US-10-348-052-22 | Sequence 22, Appl |
| 3 | 1962 | 97.4 | 1155 | 9 | US-09-970-516-1 | Sequence 1, Appli |
| 4 | 1962 | 97.4 | 1799 | 14 | US-10-354-358-25 | Sequence 25, Appl |
| 5 | 1944 | 96.5 | 1562 | 15 | US-10-264-237-1180 | Sequence 1180, Ap |
| 6 | 1927 | 95.6 | 1533 | 10 | US-09-933-767-90 | Sequence 90, Appl |
| 7 | 1927 | 95.6 | 1533 | 14 | US-10-023-282-90 | Sequence 90, Appl |
| 8 | 1594.5 | 79.1 | 1759 | 9 | US-09-784-810A-3 | Sequence 3, Appli |
| 9 | 1587.5 | 78.8 | 1143 | 9 | US-09-970-516-5 | Sequence 5, Appli |
| 10 | 875 | 43.4 | 2698 | 9 | US-09-817-676A-11 | Sequence 11, Appl |
| 11 | 856.5 | 42.5 | 1857 | 9 | US-09-970-516-3 | Sequence 3, Appli |
| 12 | 856.5 | 42.5 | 2380 | 14 | US-09-817-676A-13 | Sequence 13, Appl |
| 13 | 856.5 | 42.5 | 2380 | 14 | US-10-354-358-77 | Sequence 77, Appl |
| 14 | 550 | 27.3 | 2629 | 15 | US-10-348-052-24 | Sequence 24, Appl |
| 15 | 492.5 | 24.4 | 2609 | 15 | US-10-348-052-25 | Sequence 25, Appl |
| 16 | 481 | 23.9 | 480 | 9 | US-09-783-590-9248 | Sequence 4748, Ap |
| 17 | 444.5 | 22.1 | 2084 | 12 | US-10-424-599-47396 | Sequence 47396, A |
| 18 | 427 | 21.2 | 1869 | 12 | US-10-425-114-34806 | Sequence 34806, A |
| 19 | 365 | 18.1 | 296 | 9 | US-09-777-564-658 | Sequence 658, App |
| 20 | 365 | 18.1 | 296 | 14 | US-10-015-219-658 | Sequence 658, App |
| 21 | 360 | 17.9 | 199 | 9 | US-09-796-692-2905 | Sequence 2905, Ap |
| 22 | 360 | 17.9 | 199 | 14 | US-10-040-862-2905 | Sequence 2905, Ap |
| 23 | 360 | 17.9 | 199 | 15 | US-10-057-475B-2905 | Sequence 2905, Ap |
| 24 | 360 | 17.9 | 199 | 15 | US-10-154-884B-2905 | Sequence 2905, Ap |
| 25 | 305.5 | 15.2 | 832 | 14 | US-10-029-386-20952 | Sequence 20952, A |
| 26 | 300 | 14.9 | 1394 | 15 | US-10-264-049-204 | Sequence 204, App |
| 27 | 275 | 13.6 | 507 | 14 | US-10-029-386-7252 | Sequence 7252, Ap |
| 28 | 273 | 13.5 | 2014 | 12 | US-10-424-599-59419 | Sequence 59419, A |
| 29 | 268.5 | 13.3 | 1614 | 10 | US-09-969-898-9 | Sequence 9, Appli |
| 30 | 268.5 | 13.3 | 4413 | 10 | US-09-969-898-16 | Sequence 16, Appl |
| 31 | 266.5 | 13.2 | 1857 | 12 | US-10-425-114-32139 | Sequence 32139, A |
| 32 | 266.5 | 13.2 | 4432 | 15 | US-10-120-988-148 | Sequence 148, App |
| 33 | 260.5 | 12.9 | 4463 | 14 | US-10-315-597A-1 | Sequence 1, Appli |
| 34 | 255 | 12.7 | 1840 | 9 | US-09-784-810A-5 | Sequence 5, Appli |
| 35 | 228 | 11.3 | 394 | 9 | US-09-954-456-1756 | Sequence 1756, Ap |
| 36 | 223 | 11.1 | 979 | 10 | US-09-969-898-1 | Sequence 1, Appli |
| 37 | 221 | 11.0 | 639 | 15 | US-10-260-238-984 | Sequence 984, App |
| 38 | 213.5 | 10.6 | 1949 | 15 | US-10-260-238-1212 | Sequence 1212, Ap |
| 39 | 206 | 10.2 | 4004 | 10 | US-09-814-353-13777 | Sequence 13777, A |
| 40 | 198 | 9.8 | 2462 | 14 | US-10-037-270-796 | Sequence 796, App |
| 41 | 198 | 9.8 | 2462 | 15 | US-10-117-723-796 | Sequence 796, App |
| 42 | 188 | 9.3 | 428 | 15 | US-10-191-803-456 | Sequence 456, App |
| 43 | 187 | 9.3 | 1132 | 12 | US-10-425-114-32462 | Sequence 32462, A |
| 44 | 184.5 | 9.2 | 1632 | 12 | US-10-424-599-10078 | Sequence 10078, A |
| 45 | 158.5 | 7.9 | 3758 | 10 | US-09-948-820-42 | Sequence 42, Appl |

ALIGNMENTS

RESULT 1
US-09-784-810A-1
; Sequence 1, Application US/09784810A
; Patent No. US20020082203A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 10716-08
; CURRENT APPLICATION NUMBER: US/09/784,810A
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,360
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/191,261
; PRIOR FILING DATE: 2000-03-22
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 1
; LENGTH: 1600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)

Db 301 ATCCAGAGCCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGGCGCTGGCAGCTTCTTG 36

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121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
122
361 AACCATATGCTGGCTATGAGCAGGTACCAATGAGACCTCTCTGACCAACTGCACGCTA 420
141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
421 TTGCTGTGCGCGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
161 LeuArgSerPheSerValLeuSerLeuAlaThrGlyPheIleAlaAspValAspLeuGlu 180
481 CTGCGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
541 AGTGAGAGTATCGGCTGTGGGAGATGCGCTTCACTCTGGGCACCTTCTCTGCTGCTG 600
201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
601 GCAGCCCTCGCACCTACCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
221 LysThrProAlaSerProValValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG 240
661 AGACACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
241 LeuGluGlnValProSerHisTyrPheValProValProValProValProValProVal 260
721 CTGGAGGAGCAGTGCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
781 CTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
841 GCAGCTGGGCTCATCATCTGCTTACGTCGCGCGGAGTGTCTGTCGTCATGCTGCTG 900
301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
901 CCCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
961 TATGTGCGCGTGTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
341 AspGlyGluLeuMetValSerGluAlaValGlnGlnGlnGlnGlnGlnGlnGlnGlnG 360
1021 GATGGGAATTCATGTTAGCGAGCGCGTGCAGGCGCAGGTGCACCCAACTACTTCTGG 1080
361 MetValSerGlyCysValGluProProProSerTyrLysProGlnGlnMetProProPro 380
1081 ATGGTCAGTGGTGTGGTGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
381 GluGluProLeu 384
1141 GAAGAGCCCTTA 1152
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RESULT 3

IS-09-970-516-1

Sequence 1, Application US/09970516

Patent No. US20020099029A1

GENERAL INFORMATION:

APPLICANT: No. US20020099029A1artis AG

TITLE OF INVENTION: Induction of blood vessel formation through administration of

FILE REFERENCE: polynucleotides encoding sphingosine kinases

CURRENT APPLICATION NUMBER: US/09/970,516

CURRENT FILING DATE: 2001-10-04

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 1155

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1155)

OTHER INFORMATION:

US-09-970-516-1

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 6 53e-235 | Length: | 1155 |
| Score: | 1922.00 | Matches: | 375 |
| Percent Similarity: | 98.18% | Conservative: | 2 |
| Best Local Similarity: | 97.66% | Mismatches: | 7 |
| Query Match: | 97.37% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-09-784-810C-2 (1-384) x US-09-970-516-1 (1-1155)

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Qy 1 MetAspProAlaGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
Db 1 ATGGATCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Qy 21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
Db 61 CTGAACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Qy 41 LeuLeuAlaGluAlaGluLysSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
Db 121 CTTTGGCTCAGGCTGAAATCTCTTTCAGCTGATGCTCACTGAGCGCGGGAACACGCG 180
Qy 61 ArgGluLeuValArgSerGluGluLeuGlyArgTyrAspAlaLeuValMetSerGly 80
Db 181 CGGAGCTGTGTGCGGTGCGGAGGAGTGGGCGCGTGGGAGCGCTCTGGTGTGTCATGT 240
Qy 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTyrGluThrAla 100
Db 241 GACGGCTGTATGACGAGGTGTGTGACGGGCTCATGGAGCGGCTGACTGGGAGACGCG 300
Qy 101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLeu 120
Db 301 ATCCAGAAGCCCTGTGTAGCTCCCGAGCAGGCTCTGGCAACCGCTGGCAGCTTCCTTG 360
Qy 121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuThrAsnCysThrLeu 140
Db 361 AACATTATGCTGGCTATGAGCAGGTACCAATGAAGACCTCTCTGACCAACTGCACGCTA 420
Qy 141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
Db 421 TTGCTGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 161 LeuArgSerPheSerValLeuSerLeuAlaThrGlyPheIleAlaAspValAspLeuGlu 180
Db 481 CTGCGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
Db 541 AGTGAGAGTATCGGCTGTGGGAGATGCGCTTCACTCTGGGCACCTTCTCTGCTGCTG 600
Qy 201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
Db 601 GCAGCCCTCGCACCTACCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 221 LysThrProAlaSerProValValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG 240
Db 661 AGACACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Qy 241 LeuGluGlnValProSerHisTyrPheValProValProValProValProValProVal 260
Db 721 CTGGAGGAGCAGTGCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy 261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
Db 781 CTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
Db 841 GCAGCTGGGCTCATCATCTGCTTACGTCGCGCGGAGTGTCTGTCGTCATGCTGCTG 900
Qy 301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
Db 901 CCCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Qy 321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
Db 961 TATGTGCGCGTGTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Qy 341 AspGlyGluLeuMetValSerGluAlaValGlnGlnGlnGlnGlnGlnGlnGlnGlnG 360
Db 1021 GATGGGAATTCATGTTAGCGAGCGCGTGCAGGCGCAGGTGCACCCAACTACTTCTGG 1080
Qy 361 MetValSerGlyCysValGluProProProSerTyrLysProGlnGlnMetProProPro 380
Db 1081 ATGGTCAGTGGTGTGGTGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Qy 381 GluGluProLeu 384
Db 1141 GAAGAGCCCTTA 1152
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QY 281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
Db 841 GCAGCTGGCGTCATGATCTGTCTCTAGTGGCGGGAGTGTCTGTGTCATGCTGCTG 900
QY 301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
Db 901 CGCCTCTTCCTGGCCATGGAGAGGGCAGGCATATGGAGTATGATGATGATGATGATG 960
QY 321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
Db 961 TATGTGGCGGTGGTGGCTTCCGCTTGGAGCCCAAGATGGGAAGTGTGTGTGAGTG 1020
QY 341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAenTyrPheTyr 360
Db 1021 GATGGGAAATGATGGTAGCGAGCGGTGCGAGGCCAGGTGCACCAACTACTTCTG 1080
QY 361 MetValSerGlyCysValGluProProSerTyrPheProGlnMetProProPro 380
Db 1081 ATGTGTACGGTGTGGTGGAGCCCCCGAGCTGGAAGCCCGCAGCAGATGCCACCGCCA 1140
QY 381 GluGluProLeu 384
Db 1141 GAAGAGGCCCTTA 1152

RESULT 4
US-10-354-358-25
; Sequence 25, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lescon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21325, 1420, 32236, 2039,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 64628 MOLECULES
; FILE REFERENCE: NPI02-020P1RNOWNIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; REMAINING Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1799
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (359)...(1513)
US-10-354-358-25

Alignment Scores:
Pred. No.: 1,276-234 Length: 1799
Score: 1962.00 Matches: 375
Percent Similarity: 98.18% Conservatives: 2
Best Local Similarity: 97.66% Mismatches: 7
Query Match: 97.37% Indels: 0
DB: 14 Gaps: 0

US-09-784-810C-2 (1-384) X US-10-354-358-25 (1-1799)
QY 1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
Db 359 ATGGATCCAGCGGGCGGCCCGCGGGCGTGTCTCCCGGGCGCTCGCGGTCTGTGTGTG 418
QY 21 LeuAenProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
Db 419 CTGAACCCCGCGCGCGGCAAGGCAAGGCCCTTGAGCTCTTCCGGAGTCACGTGCAGGCC 478
QY 41 LeuLeuAlaGluAlaGluLeuSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
Db 479 CTTTTGGCTGAGGCTGAATCTCTTACGGCTGATGCTCACTGAGCGCGGAAACACCGCG 538
QY 61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAlaLeuValValMetSerGly 80
Db 539 CGGAGCTGGTGGTGGTGGAGAGTGGCGCGCTGGGACGCTCTGGTGGTCTGTGTGGA 598
QY 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
Db 599 GACGGCTGTATGACAGAGTGTGTACGGGCTCATGGAGCGGCTGACTGGAGAGCGGCC 658
QY 101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLeu 120
Db 659 ATCCAGAGAGCCCTGTGTAGCTCCAGCAGCTCTGGCAACGCGCTGGCAGCTTCCTTG 718
QY 121 AsnHisTyrAlaGlyTyrGluValThrAsnGluLeuLeuThrAsnCysThrLeu 140
Db 719 AACCATTTATGTGGTATGACAGAGTCAACATGAAGACCTCTCTGACCACTGCACGCTA 778
QY 141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
Db 779 TTGCTGTGCGCGCGCTGCTGTACCCATGAACCTGTCTCTGCACACGCTTCGGGG 838
QY 161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
Db 839 CTGGCGCTCTTCTCTGTGCTCAGCTGGCGCTGGGGCTTCAITGTGATGTGGACCTAGAG 898
QY 181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
Db 899 AGTGAGAGATATCGCGCTCTGGGGGAGATGCGTTCCTCTGGGCACCTCTCTGCTGTG 958
QY 201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
Db 959 GCAGCCCTCGCGACCTACCGCGCGGCGACTGGCCCTACCTCCCTGTAGGAAGAGTGGGTCC 1018
QY 221 LysThrProAlaSerProValValGlnGlnGlyProValAspAlaHisLeuValPro 240
Db 1019 AAGACACCTGCTCCCGCTTGTGTCTCAGCAGGCGCGGTAGATGCACACTTGTGCCA 1078
QY 241 LeuGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
Db 1079 CTGGAGGAGCCAGTCCCTCTCACTGGACAGTGGTGGCGCGAGGAGCTTTGTGTAGTTC 1138
QY 261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
Db 1139 CTGGACATGCTGCACTCGACCTGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1198
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2y 281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
2b 1199 GAGCTGGCGTCAATGCTTACGTCGCGGGGAGTCTCGTGCCATGCTGCTG 1258
2y 301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
2b 1259 CGCTCTTCTCGCCATGAGAAAGGCGAGGCATATGGAGTATGAATGCCCTTACTTTGTA 1318
2y 321 TyrValProValAlaPheArgLeuGluProLysAspGlyValPheAlaVal 340
2b 1319 TATGTCGCGTGGCTTCCGCTTGGAGCCCAAGGATGGAAAGGTGTGTTGCAGTG 1378
2y 341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTyr 360
2b 1379 GATGGGAATTGATTGTTAGCGAGCGCTGACGGCCAGGTGCACCCAACTACTTCTGG 1438
2y 361 MetValSerGlyCysValGluProProSerTyrLysProGlnGlnMetProProPro 380
2b 1439 ATGGTCAGCGGTGCGTGAGCGCCCGCCAGCTGGAAAGCCCGCAGCAGATGCCACGCCA 1498
2y 381 GluGluProLeu 384
2b 1499 GAAGAGCCCTTA 1510

RESULT 5

US-10-264-237-1180/c
Sequence 1180, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1180
LENGTH: 1562
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(7)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(12)
OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1180

Alignment Scores:
Seq. No.: 1,836-232 Length: 1562
Score: 1944.00 Matches: 372
Percent Similarity: 98.16% Conservative: 2
Best Local Similarity: 97.64% Mismatches: 7
Query Match: 96.48% Indels: 0
B: 15 Gaps: 0

S-09-784-810C-2 (1-384) x US-10-264-237-1180 (1-1562)

y 4 AlaGlyProArgGlyValLeuProArgProCysArgValLeuValLeuLeuAsnPro 23
b 1453 GCGGGCGGCGCCCGGGGTGCTCCCGCGCCCTCCGCGTCTGGTCTGCTGAACCCG 1394
y 24 ArgGlyGlyLysGlyValAlaLeuGlnPheArgSerHisValGlnProLeuLeuAla 43
b 1393 CCGGGCGGCAAGGCAAGCCCTTGAGCTCTTCCGAGTCAGTCGACCCCTTTTGCT 1334
y 44 GluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeu 63

Db 1333 GAGCTGAATCTCCTTTCACGCTGATGCTCACTGAGCGCGGAACACACGCGCGGAGCTG 1274
Qy 64 ValArgSerGluGluLeuGlyArgTyrAspAlaLeuValValMetSerGlyAspGlyLeu 83
Db 1273 GTGGGTGCGAGGAGCTGGGCCCTGGGACGCTCTGGTGTCTATGCTGGAGACGGGCTG 1214
Qy 84 MethIsgluValAlaAndGlyLeuMetGluArgProAspTyrGluThrAlaIleGlnLys 103
Db 1213 ATGCACAGGTGGTGAACGGGCTCATGGAGCGGCTGACTGGGAGACCGCCATCCAGAAG 1154
Qy 104 ProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyr 123
Db 1153 CCCTGTGTAGCTCCACGAGGCTCTGGCAACGCGCTGGCAGCTTCTTGAACCATAT 1094
Qy 124 AlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCys 143
Db 1093 GCTGGCTATGAGGAGGTCAACAATGAAGACCTCTCTGCAACCTGACGCTATTGCTGTGC 1034
Qy 144 ArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSer 163
Db 1033 CGCGGCTGTGTACCCATGAACCTGTGCTCTGCACACGCGCTTCGGGGCTCGGCTC 974
Qy 164 PheSerValLeuSerLeuAlaTyrGlyPheIleAlaAspValAspLeuGluSerAspLys 183
Db 973 TTCTCTGTCTCAGCTGGCTGGGCTTCATTGCTGATGTGACCTAGAGAGTGAAG 914
Qy 184 TyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeu 203
Db 913 TATCGGCTGTGGGGAGATGCGCTTCACTCTGGGACCTTCTCTGCTGGCAGCCCTG 854
Qy 204 ArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPheLysThrPro 223
Db 853 CGCACCTACCGCGCGCTGCTGCTACCTCCCTGTAGGAAGAGTGGGTTCCTGAAGACCT 794
Qy 224 AlaSerProValValGlnGlnGlyProValAspAlaHisLeuValProLeuGluGlu 243
Db 793 GCCTCCCGCTGTGTGTCAGAGCGCCCGGTAGATGCACACCTTGTGCACCTGGAGGAG 734
Qy 244 GlnValProSerHisTyrGlnValValProAspGluAspPheValLeuValLeuAlaLeu 263
Db 733 CCAGTGCCTCTCACTGGACAGTGGTGGCGGAGGAGCTTTGTGTAGTCTCTGGCACTG 674
Qy 264 LeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCysAlaAlaGly 283
Db 673 CTGCACCTCGCACCTGGCGAGTGGATGTTTGTGTCACCCATGGCGCGCTGTGCACTGGC 614
Qy 284 ValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeuArgLeuPhe 303
Db 613 GTATGCACTGTTCTACGTGCGGGCGGAGGTCTCTGTCCTATGCTGTCGCGCTCTTC 554
Qy 304 LeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuValTyrValPro 323
Db 553 CTGGCCATGGAGAAGGCGAGGCATATGGAGTATGAATGCCCTACTTGTGTATATGTGCC 494
Qy 324 ValValAlaPheArgLeuGluProLysAspGlyValPheAlaValAspGlyGlu 343
Db 493 GTGTCGCTTCCGCTTGGAGCCCAAGGATGGAAAGGTGTGTTTCAGTGGATGGGAA 434
Qy 344 LeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTyrMetValSer 363
Db 433 TTGATGTTAGCGAGCGCTGCGAGGCCAGGTGCACCCAACTACTTCTGATGGTGCAGC 374
Qy 364 GlyCysValGluProProProSerTyrLysProGlnGlnMetProProProGluGluPro 383
Db 373 GGTGTGGTGGAGCCCCCGCCAGCTGGAAGCCCCAGATGCCACCGCAGGAAGACCC 314
Qy 384 Leu 384
Db 313 TTA 311
RESULT 6
US-09-933-767-90

; Sequence 90, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
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; PRIOR FILING DATE: 1997-06-06
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; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949

; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
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; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1522)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1527)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-933-767-90
Alignment Scores:
Pred. No.: 2,37e-230 Length: 1533
Score: 1927.00 Matches: 371
Percent Similarity: 96.88% Conservative: 2
Best Local Similarity: 96.38% Mismatches: 11
Query Match: 95.63% Indels: 1
DB: 10 Gaps: 0

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| 193 | CTTTTGGCTAGGCTGAATCTCTCTTCA | CGCTGATGCTCACTGAGCGCGGAAACACGCG | 252 |
| 61 | ArgGluLeuValArgSerGluGluLeuGlyArgT | ProAspAlaLeuValValMetSerGly | 80 |
| 253 | CGGARGCTGGTGGGTCGAGAGCTGGCCGCTG | GRACGCTCTGCTGTCATGTTGGA | 312 |
| 81 | AspGlyLeuMetHisGluValValAa | AndGlyLeu-MetGluArgProAspT | 100 |
| 313 | GACGGGCTGATGACAGAGTGTGTAA | CGGGCTTCATGGAGCGGCTTGATGGGAGACCGC | 372 |
| 100 | alleGlnLysProLeuCySerSerLeuPro | AlaGlySerGlyAsnAlaLeuAlaSerLe | 120 |
| 373 | CATCCAGAAAGCCCTGTGTAGCCTCC | CACAGGCTCTGGCAAGCGCTGGAGTTCCTT | 432 |
| 120 | uAenHisTyrAlaGlyTyrGluGlnVal | ThrAenGluAspLeuLeuThrAsnCysThrLe | 140 |
| 433 | RAACCAATTATGCTGGCTATPAGCAGGT | CAACATGAAGACCTCTCTGACCACTGACGCT | 492 |
| 140 | uLeuLeuCysArgProValLeuSerPro | MetAsnLeuLeuSerLeuHisThrAlaSerG | 160 |
| 493 | ATTGCTGTGGCCGCGCTGCTGTACCC | ATGAACTGCTGTCTCTGCACACGGCTTCGGG | 552 |
| 160 | yLeuArgSerPheSerValLeuSerLeu | AlaThrGlyPheLeuAlaAspValAspLeuG | 180 |
| 553 | GCTGCGCCTCTTCTCTGTGCTCAGCC | TGGCCTGGGCTTCATTGTGTGATGTGGACCTAG | 612 |
| 180 | uSerAspLysTyrArgArgGluGlyGlu | MetArgPheThrLeuGlyThrPheLeuArgLe | 200 |
| 613 | GAGTGAAGATTCGGCGCTCTGGGGAG | ATGGCTTCATCTTGGGCACTCTCTCGGTCT | 672 |
| 200 | uAlaAlaLeuArgThrTyrArgLysArg | LeuAlaThrLeuProValGlyArgValGlyPh | 220 |
| 673 | GGCAGCCCTGGCACCTACCGGGCGC | AGTGGCCTACCTCCCTGTAGGAAGAGTGGGTT | 732 |
| 220 | eLysThrProAlaSerProValValGln | GlnGlyProValAspAlaHisLeuValPr | 240 |
| 733 | CAAGACACTGCTCCCCGTTGTGTGT | CCAGAGGCGCGGTAGATGCACACTTGTGCC | 792 |
| 240 | oLeuGluGluGlnValProSerHisT | ProGlnValValProAspGluAspPheValLeuVa | 260 |
| 793 | ACTGGAGAGCCAGTGCCTCTC | ACTGGACAGTGGTCCCGACGAGACTTTGTGCTAGT | 852 |
| 260 | lLeuAlaLeuLeuHisSerHisLeu | AlaSerGluMetPheAlaAlaProMetGlyArgCy | 280 |
| 853 | CCTGGACACTGCTGCATCGAC | CTGCACCTGGGCAGTGGATGTTGTGTGCACCCATGGCCGCTG | 912 |
| 280 | sAlaAlaGlyValMetHisLeuPheTyr | ValArgAlaGlyValSerArgAlaMetLeuLe | 300 |
| 913 | TGCAGCTGGCGTCATGCATCTGTT | CTACGTGGCGCGGAGTGTCTCTGTGCCATGTGCTGT | 972 |
| 300 | uArgLeuPheLeuAlaMetGluLysGly | ArgHisMetGluTyrGluCyProTyrLeuVa | 320 |
| 973 | GCGCCCTCTCTGGCCCATGGAGA | AGGCGCATATGGAGTATGAATGCCCTTACTTGGT | 1032 |
| 320 | lTyrValProValValAlaPheArgLeu | GluProLysAspGlyLysGlyValPheAlaVa | 340 |
| 1033 | ATATGTGCCCGGTGCGCTTCCGCT | TGGAGCCCAAGGATGGGAAGGTGTGTTCGAGT | 1092 |
| 340 | lAspGlyGluLeuMetValSerGluAla | ValGlnGlyGlnValHisProAsnTyrPheTr | 360 |
| 1093 | GGATGGGAATTGATGGTTAGCGAGG | CCGTGACAGGCCAGGTGCACCCAACTACTTCTG | 1152 |
| 360 | pMetValSerGlyCysValGluProPro | SerTyrLysProGlnGluMetProProPr | 380 |
| 1153 | GATGGTCACGGTTCGTGGAGCCCC | CGCCAGCTGGAAAGCCCCCAGCAGATGCCACCGCC | 1212 |
| 380 | oGluGluProLeu | 384 | |
| 1213 | AGAGAGCCCTTA | 1225 | |

RESULT 8
 US-09-784-810A-3
 Sequence 3, Application US/09784810A

```
; Patent No. US20020082203A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
; FILE OF INVENTION: SAME
; FILE REFERENCE: 10716-08
; CURRENT APPLICATION NUMBER: US/09/784,810A
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,360
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/191,261
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1759
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-784-810A-3

Alignment Scores:
Pred. No.: 1,08e-188 Length: 1759
Score: 1594.50 Matches: 303
Percent Similarity: 88.25% Conservative: 35
Best Local Similarity: 79.11% Mismatches: 44
Query Match: 79.13% Indels: 1
DB: 9 Gaps: 1

US-09-784-810C-2 (1-384) x US-09-784-810A-3 (1-1759)

2y 1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
2b 327 ATGGAACCAAGTAGAATGCCCTCGAGAGCTGCTCCACAGGCCATGAGAGTGTGCTG 386
2y 21 LeuAsnProArgGlyGlyValLeuValLeuValLeuValLeuValLeuValLeu 40
2b 387 CTGAACCCAGGCTGCGAGGCAAGGCTGCGAGCTCTCCAGAGCGGTGCGAGCCC 446
2y 41 LeuLeuAlaGluAlaGluLeuSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
2b 447 TTCTCGAGAGGAGCAGAGATAACCTTTAACTGATACCTACCGACGGAAGAACCATGCC 506
2y 61 ArgGluLeuValArgSerGluGluLeuGlyValArgTrpAspAlaLeuValValMetSergly 80
2b 507 AGGAGACTGGTGTGTCAGAGAGTTGGGTCACTGGGACGCCCTCGGAGTCTATGTCGGT 566
2y 81 AspGlyLeuMetHisGluValValAenGlyLeuMetGluArgProAspTrpGluThrAla 100
2b 567 GATGGTCTGATGATGAAGTGTGATGAGTGAATGAGTGAATGAGTGAATGAGTGAATG 626
2y 101 IleGlnProLeuGlySerLeuProAlaGlySerGlyAsnAlaLeuAlaLeuSerLeu 120
2b 627 ATCCAGAAACCCCTGTAGTACCTCCCTGGAGGCTCCGCAATGCTGCGAGCTTCTGTG 686
2y 121 AsnHisTyAlaGlyTyArgGluValValTrpAsnGluValLeuThrAsnCysThrLeu 140
2b 687 AACCACTATGCTGGTACGAGAGGAGTATGAGACCTGCTCATCACTGACACTG 746
2y 141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerHisThrAlaSergly 160
2b 747 CTGTTGTGCGCGCGGCTGTACCCATGAACCTGTCTCCCTGCACACTGCTTCTGGG 806
2y 161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
2b 807 CTGCGGCTCTATTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 866
2y 181 SerAspLysTyArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
2b 867 AGTGAGAGTACAGGCGCTTGGGGAGATTCCTTTCACAGTGGGCACTTCTTTCGCTA 926
2y 201 AlaAlaLeuArgThrTyArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
2b 927 GCAAGCCTGCGATCTACCAAGGCCCACTGGGCTACCTTCTCTAGGAACCTGTGCGCTCT 986

; LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240
; 987 AAGAGACCGGCTCT--ACACTGGTGAGAAAGGCGCCGCTCGACACACACTTGTCTCT 1043
;
; LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
; 1044 CTGAGAGGAGCCAGTGCCTTCTCATGTGACTGTGTGTACAGACAGGACTTGTCTGTG 1103
;
; LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
; 1104 CTGGTGTGTGTACACACCCACCTGAGCTCCGAGCTGTTTGCAGACCCATGGCGGCTGT 1163
;
; AlaAlaGlyValMetHisLeuPheTyValArgAlaGlyValSerArgAlaMetLeuLeu 300
; 1164 GAGCTGTGTGTATGTCATCTGTTCTACGTAGCTGCGGGGGTGTCAAGGGCTGCGCTGT 1223
;
; ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyArgCysProTyLeuVal 320
; 1224 CGCTCTTCTGCGCATGTCAGAGGCAAGCATATGAACTTGACTGTCCATACCTGTT 1283
;
; TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
; 1284 CATGTGCGCGTGTGTGCTTCCGCTCGAGCCCGAGGAGGAGGCGGCTGTTTCTGTG 1343
;
; AspGlyGluLeuMetValSerGluAlaValGlnGlnValHisProAsnTyPheTrp 360
; 1344 GATGAGAGCTGATGTTGTGAGCTGTGAGGCGCAAGTGCACCCAACTACTCTTGG 1403
;
; MetValSerglyCysValGluProProSerTrpLysProGlnGlnMetProProPro 380
; 1404 ATGCTGTGTGCGAGAGATGCCCATCCGCGCGGAGCTCCCGCGGCGGCGGCGGCTCCA 1463
;
; GluGluPro 383
; 1464 GAGAACCA 1472

RESULT 9
US-09-784-810C-2 (1-384) x US-09-784-810A-3 (1-1759)
; Sequence 5, Application US/09970516
; Patent No. US20020099029A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020099029A1artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 5
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1149)
; OTHER INFORMATION:
; US-09-784-810C-2 (1-384) x US-09-784-810A-3 (1-1759)

Alignment Scores:
Pred. No.: 4,28e-188 Length: 1149
Score: 1587.50 Matches: 302
Percent Similarity: 87.99% Conservative: 35
Best Local Similarity: 78.85% Mismatches: 45
Query Match: 78.78% Indels: 1
DB: 9 Gaps: 1

US-09-784-810C-2 (1-384) x US-09-784-810A-3 (1-1759)

2y 1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
2b 1 ATGGAACCAAGTAGAATGCCCTCGAGAGCTGCTCCACAGGCCATGAGAGTGTGCTGCTG 60
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QY 21 LeuAsnProArgGlyGlyValysGlyValAlaLeuGlnLeuPheArgSerHisValGlnPro 40
Db 61 CTGAACCCCGAGGGTGGCAAGGGCAAGGCTCTGAGGCTCTCCAGAGCCGTGGAGCCC 120
QY 41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
Db 121 TTCTGAGGAGGAGCAGATAACTTTAACTGATCTACCGAAGCAAGCAACCATGCC 180
QY 61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValMetSerGly 80
Db 181 AGGAGCTGGTGTGTCAGAGGAGTGGGTGACCTGGGAGCCCTGGCAGTCATGTCGGT 240
QY 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
Db 241 GATGCTGATGATGAGTGGTGAATGGCTAATGGAAACGGCCGACCTGGGAGACTGCC 300
QY 101 IleGlnIysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLeu 120
Db 301 ATCCAGAAACCCCTGTAGCTCCCTGGAGGCTCCGGCAATCGCTGGCAGCTTCTGTG 360
QY 121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
Db 361 AACCACTATGCTGGTACGAGCAGGTGACTAATGAGACCTGCTCATCACTGCACACTG 420
QY 141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
Db 421 CTGTGTGTCGCGCGCGCTGTCCACCATGAACCTGCTGTCCTGCACACTGCTTCTGG 480
QY 161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
Db 481 CTGCGGCTATCTGTCAGTCTGCTGCGGCTTGTGTCAGCTGGACCTGCGAG 540
QY 181 SerAspIysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
Db 541 AGTGAGAGTACAGCGCTTGGGGAGATCTGTTTACAGTGGGCGACCTTCTTTCGCTA 600
QY 201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
Db 601 GCAAGCTGGCATCTACCAAGGCCAATCGGCTACCTCTCTAGAACTGGGCGCTCT 660
QY 221 LysThrProAlaSerProValValGlnGlnGlyProValAspAlaHisLeuValPro 240
Db 661 AAGAGACCCGCTCT--ACACTGGTCCAGAGGGCCCTGTCACACACACCTTGTCTCT 717
QY 241 LeuGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
Db 718 CTGAGGAGGCGAGTGGCTTCTCATTTGACTGTGTACCAAGACGAGACTTTGTCTCTG 777
QY 261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
Db 778 CTGGTGTGTACACACCCACCTGAGCTCCGAGCTGTTTGCACACACCATGGGCCCTGT 837
QY 281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
Db 838 GAGGCTGGTGTATGATCTGTTCTAGCTACGTGCGGGGGTGTCAAGGGCTGGCTGCTG 897
QY 301 ArgLeuPheLeuAlaMetGluIysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
Db 898 CGCTCTTCTCCGCGCATGCGAAGGGCAAGCATATGGAATTCAGCTGTCATACCTGGTT 957
QY 321 TyrValProValValAlaPheArgLeuGluProIlysAspGlyIysGlyValPheAlaVal 340
Db 958 CATGTGCCCGTGGTGTCTTCCGCTCGAGGCCAGGAGCCAGGGCGTGTCTTCTGTG 1017
QY 341 AspGlyGluLeuMetValSerGluAlaValGlnGlnValHisProAsnTyrPheTrp 360
Db 1018 GATGAGGGCTGTATGGTATGAGAGCTGTGCGAGGCCCAAGTGCACCCAACTACCTTTGG 1077
QY 361 MetValSerGlyCysValGluProProSerTrpIysProGlnGlnMetProProPro 380
Db 1078 ATGCTCTGTGCACAGAGATGCCCATCGGCGCGGACTCCCGGGGGGGCCACCTCCA 1137

QY 381 GluGluPro 383
Db 1138 GAAGAACCA 1146
RESULT 10
US-09-817-676A-11
; Sequence 11, Application US/09817676A
; Patent No. US20020042101A1
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; APPLICANT: Kohama, Takafumi
; TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
; TITLE OF INVENTION: Expression and Methods of Use Thereof
; FILE REFERENCE: 00170/HG
; CURRENT APPLICATION NUMBER: US/09/817,676A
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/194,318
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2698
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (387)..(2237)
; PUBLICATION INFORMATION:
; TITLE: Molecular cloning and functional characterization of a
; TITLE: novel mammalian sphingosine kinase type 2 isoform
; JOURNAL: J. Biol. Chem.
; VOLUME: 275
; ISSUE: 26
; PAGES: 19513-19520
; DATE: 2000-06-30
; DATABASE ACCESSION NUMBER: AF245448
; DATABASE ENTRY DATE: 2000-06-27
US-09-817-676A-11
Alignment Scores:
Pred. No.: 1,84e-98 Length: 2698
Score: 875.00 Matches: 187
Percent Similarity: 51.98% Conservative: 63
Best Local Similarity: 38.98% Mismatches: 111
Query Match: 43.42% Indels: 120
DB: 9 Gaps: 4
US-09-784-810C-2 (1-384) x US-09-817-676A-11 (1-2698)
QY 10 ValLeuProArgProCysArgValLeuValLeuLeuAsnProArgGlyGlyValysGlyLys 29
Db 807 TTGCTGCCCGGAGAGCCAGGCTGCTCATATTTGTCATCCCTTTGGGGGGGGGCTG 866
QY 30 AlaLeuGlnLeuPheArgSerHisValGlnProLeuLeuAlaGluAlaGluIleSerPhe 49
Db 867 GCTTGGCAGCGCTGTATGACACCGCTGTCATGATCTCTGAAGCTGGGCTCTCCTTC 926
QY 50 ThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeu 69
Db 927 AACCTCATACAGACAGAACCATGCCCTGAGCTGGTGAGGGGTTAAGCCTG 986
QY 70 GlyArgTrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsn 89
Db 987 AGTGAGTGGGAAGGCAATGTCTACGTGTCTGACACCGGCTGCTTACGAGGTCTGTAAT 1046
QY 90 GlyLeuMetGluArgProAspTrpGluThrAlaIleGlnIysProLeuCysSerLeuPro 109
Db 1047 GGGCTCTTGTATGCGCCAGACTGGAGAGATGCCCTGGGATGCCCATTTGTGTCTCCCC 1106
QY 110 AlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
Db 1107 TGTGATCGGCAATGCTAGCTAGCTGGGCGGTGAGCCATCATGCGGGTTTGACAGGTT 1166


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db 964 GCGCGCTTCACACTGGGACGGTGTGGCGCTTGGCCACTGCACACTGACCGGACGC 1023
2y 210 LeuAlaThrLeuProVal
db 1024 CTCCTCTACTCTCCCGCCACTGTGGAACTGCTGCCGCCACCCCTGCCATAGCTGTGCT 1083
2y 215 -----
db 1084 CGTGCCAAGTCGAGCTGACCTTAACCCAGACCCCGCCGCTGCTGCTGCTGCTGCT 1143
2y 215 -----
db 1144 CTGCATGTTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1203
2y 215 -----
db 1204 GGCTGCCAGAACCCCTGCCATCTGCTCCCTCAAGGTGGGGGCCAGAGCTGCTGGG 1263
2y 215 -----
db 1264 GACTGGGGTGGGGCTGGGATGCTCGCTGTCCCGGACCCACTGCTGCTTCACTGCT 1323
2y 216 -----GlyArgValGlyPheLysThrProAlaSer-----ProValValValGln 230
db 1324 GGCTCTCCAGGAGCTCTACACTACCCGCTCTCCGAGGGGGCCCGTAATCCCCCA 1383
2y 231 Gln-----
db 1384 TCCTCTGGCTCCCACTTCCCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1443
2y 234 ValAspAlaHisLeuValProLeuGluGluGlnValProSerHisTrrpGlnValValPro 253
db 1444 CCGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
2y 254 AspGluAspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPhe 273
db 1501 GAGGGGACTTTGTCTCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
2y 274 AlaAlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGly 293
db 1561 GCAGCTCCCGCATGCGCGCTTCGACGACGCGCTGTGTCACCTGTGCTGCTGCTGCTG 1620
2y 294 ValSerArgAlaMetLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 313
db 1621 ATCTCGGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
2y 314 TyrGluCysProTyrLeuValTyrValProValAlaPheArgLeuGluProLysAsp 333
db 1681 CTGGGCTGTCCGAGCTGGGCTACGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
2y 334 GlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGlyGln 353
db 1741 CCACGCGGCTGCTCACAGTGGACGGGAGCAGGTGGAGTATGGGCCGCTACAGCACAG 1800
2y 354 ValHisProAsnTyrPheTrrpMetValSerGlyCysValGluProProSerTrrpLys 373
db 1801 ATGCACCTGGCATGGTACATGCTCACTGG-----CTTCTGGGTGC----- 1845
2y 374 ProGlnGlnMetProProGluGluPro 383
db 1846 -----CCGGGGGGGAGGCC 1860
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RESULT 13

US-10-354-358-77

Sequence 77, Application US/10354358

Publication NO. US20030157082A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc

APPLICANT: Hunter, John Joseph

APPLICANT: MacBeth, Kyle J.

APPLICANT: Tsai, Fong-ying

APPLICANT: Lesoon, Andrea

APPLICANT: Lightcap, Eric S.

```
APPLICANT: Williamson, Mark
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 140, 1470, 1886, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
FILE REFERENCE: ME102-020PKNOMNIM
CURRENT APPLICATION NUMBER: US/10/354,358
CURRENT FILING DATE: 2003-01-30
PRIORITY APPLICATION NUMBER: US 60/353,600
PRIORITY FILING DATE: 2002-01-31
PRIORITY APPLICATION NUMBER: US 60/364,517
PRIORITY FILING DATE: 2002-03-15
PRIORITY APPLICATION NUMBER: US 60/371,075
PRIORITY FILING DATE: 2002-04-09
PRIORITY APPLICATION NUMBER: US 60/371,507
PRIORITY FILING DATE: 2002-04-10
PRIORITY APPLICATION NUMBER: US 60/372,984
PRIORITY FILING DATE: 2002-04-16
PRIORITY APPLICATION NUMBER: US 60/374,194
PRIORITY FILING DATE: 2002-04-19
PRIORITY APPLICATION NUMBER: US 60/382,995
PRIORITY FILING DATE: 2002-05-24
PRIORITY APPLICATION NUMBER: US 60/385,023
PRIORITY FILING DATE: 2002-05-31
PRIORITY APPLICATION NUMBER: US 60/388,853
PRIORITY FILING DATE: 2002-06-14
PRIORITY APPLICATION NUMBER: US 60/389,395
PRIORITY FILING DATE: 2002-06-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 77
LENGTH: 2380
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (7)...(1863)
US-10-354-358-77
Alignment Scores:
Pred. No.: 3,13e-96 Length: 2380
Score: 856.50 Matches: 189
Percent Similarity: 51.43% Conservative: 63
Best Local Similarity: 38.57% Mismatches: 111
Query Match: 42.51% Indels: 127
DB: 6 Gaps: 6
US-09-784-810C-2 (1-384) x US-10-354-358-77 (1-2380)
Qy 10 ValLeuProArgProCysArgValLeuValLeuAsnProArgGlyGlyLysLys 29
Db 424 CTGCTACTCGCGCGCGCGCTTCTATTGTCATCCCTTTGGGGTCCGGGCGCTG 483
Qy 30 AlaLeuGlnLeuPheArgSerHisValGlnProLeuLeuAlaGluAlaGluIleSerPhe 49
Db 484 GCCTGGCAGTGGGTGAAGAACACACGCTCTCCCATGATCTCTGAAGCTGGGCTCTTC 543
Qy 50 ThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeu 69
Db 544 AACCTTCATCCAGACAGAACACAGAACACACGCGCGGAGCTGGTCCAGCGGCTGAGCCTG 603
Qy 70 GlyArgTrrpAspAlaLeuValValMetSerGlyLysGlyLeuMetHisGluValValAsn 89
Db 604 AGTGAGTGGGATGGCATCGCTACCGGTCTCGGAGACGGGCTGCTCATGAGGTGCTGAAC 663
Qy 90 GlyLeuMetGluArgProAspTrrpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
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Db 664 GGGCTCCTAGATCGCCCTGACTGGAGGAAGCTGTGAAGATGCTGTGGGCATCTCTCCCC 723
Qy 110 AlaGlySerGlyAsnAlaLeuAlaAaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
Db 724 TGGGGCTCGGGCAACGGCTGGCGGGAGAGTGAACAGCAGCGGGGATTTGAGCAGCC 783
Qy 130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
Db 784 CTGGGCTCGACCTGTGCTCACTGCTCACTGTGCTGCTGGGGGTGGTGGCCACCCA 843
Qy 150 MetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSerLeu 169
Db 844 CTGACCTGTCTCCGAGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 903
Qy 170 AlaTyrGlyPheLeuAlaAspValAspLeuGluSerAspTyrArgLeuGlyGlu 189
Db 904 GCCTGGGGCTCTGCTGATGTGATATCCAGAGGAGCGCTTCAGGGCTTGGGAGT 963
Qy 190 MetArgPheThrLeuGlyThrPheLeuArgLeuAlaLeuArgThrTyrArgGlyArg 209
Db 964 GCCCGCTTCACTGGGCGAGGTGCTGGGCTGGCCACACTGCACACCTACCGCGGACGC 1023
Qy 210 LeuAlaThrLeuProVal----- 215
Db 1024 CTCCTCTACTCTCCCGCCACTGTGGAACTGCTGCGCCACCCCTGCGCCCATACCTGCCT 1083
Qy 215 ----- 215
Db 1084 CGTGCCAAAGTCGAGTGACCTAAACCCAGACCCAGCCCGCCCATGGGCCACTCACCC 1143
Qy 215 ----- 215
Db 1144 CTGCATCTCTGTGTCTGACTGCTCTTCCCTGCTCCCGAGCGCTGGCTGCTCTCTCT 1203
Qy 215 ----- 215
Db 1204 GGCTGCCAGAACCCCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1263
Qy 215 ----- 215
Db 1264 GACTGGGGTGGGGTGGGATGCTCCGCTGTCCCGGAGCCACTGCTGTCTTCCACTCTCT 1323
Qy 216 -----GlyArgValGlyPheLeuThrProAlaSer-----ProValValGln 230
Db 1324 GGCTCTCCCAAGGAGCTCTACACTACCCGCTCTCCGAGGGGCCCCGPAATCTCCCA 1383
Qy 231 Gln-----GlyPro 233
Db 1384 TCCTCTGGGCTCCCACTTCCACCCCTGATGCGCGGTAGGGGCTCCACTCGGCCCG 1443
Qy 234 ValAspAlaHisLeuValProLeuGluGlnValProSerHisThrPheGlnValPro 253
Db 1444 CCCGACCACTGCTGCTGCTGCTGGGACCCCGCTGGGACCCCGCTGGGACCTGG 1500
Qy 254 AspGluAspPheValLeuValLeuAlaLeuHisSerHisLeuAlaSerGluMetPhe 273
Db 1501 GAGGGGACTTTGTGCTCATGTGTGGCCATCTGCGCCAGCCACTAGCGCTGACTGGTG 1560
Qy 274 AlaAlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGly 293
Db 1561 GCAGCTCGCATGTCGCGCTTCGACGAGCGGCTGTGTGACCTGTGCTGGTGGTGGC 1620
Qy 294 ValSerArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLeuGlyArgHisMetGlu 313
Db 1621 ATCTCGGGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Qy 314 TyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLysAsp 333
Db 1681 CTGGGCTGTCCGACAGTGGGCTACCGCGGCGCGCTGCTTCCGCTTAGAGCGCTCACA 1740
Qy 334 GlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGlyGln 353
Db 1741 CCACGGCGGCTGCTCACAGTGGAGCGGAGCGAGTGGAGTATGGGCGGCTACAGGCACAG 1800

Qy 354 ValHisProAsnTyrPheTyrMetValSerGlyCysValGluProProSerTyrPhe 373
Db 1801 ATGCACCTTGCATCGGTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1845
Qy 374 ProGlnGlnMetProProGluGluPro 383
Db 1846 -----CCGGGGCGGAGGCC 1860
RESULT 14
US-10-348-052-24
; Sequence 24, Application US/10348052
; Publication No. US20030219782A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Henrik
; APPLICANT: Fyret, Henrik
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
; OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
; FILE REFERENCE: 200116.405
; CURRENT APPLICATION NUMBER: US/10/348.052
; CURRENT FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-348-052-24
Alignment Scores:
Pred. No.: 7,576-58 Length: 2629
Score: 550.00 Matches: 146
Percent Similarity: 46.59% Conservative: 66
Best Local Similarity: 32.09% Mismatches: 125
Query Match: 27.30% Indels: 118
DB: 15 Gaps: 14
US-09-784-810C-2 (1-384) x US-10-348-052-24 (1-2629)
Qy 12 ProArgProCys-----ArgValLeuValLeuLeuAsnProArgGlyGlyGlyLys 29
Db 784 CCGCGGATTTGGGCAACAGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 843
Qy 30 AlaLeuGlnLeuPheArgSerHisValGlnProLeuLeuAlaGluAlaGluSerPhe 49
Db 844 GGGCTGAGCTCTTCCAGAAACAGTGGCCTTGTGACGGAAGCAGAGTGAATAC 903
Qy 50 ThrLeuMetLeuThrGluArgAsnHisAlaArgGluLeuValArgSerGluGlu 68
Db 904 GATCTCCAGATCACCACACATCCGAGTATGCCAAGGATTCGTGGCAGCAGAGGAT 963
Qy 69 ---LeuGlyArgTyrAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluVal 87
Db 964 CTGCTGACACGCTATTCGGGCAATTGTGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1023
Qy 88 ValAsnGlyLeuMetGluArgProAspTyrGluThrAlaLeuGlnLys---ProLeuCys 106
Db 1024 CTCATGGGCTAATGGAACGATGATGGCGCGGAGCTTCAGGAGCTACCGCTTGGC 1083
Qy 107 SerLeuProAlaGlySerGlyAsnAlaLeuAlaLeuAlaSerLeuAsnHisTyrAlaGly 125
Db 1084 ATTATACCATGTGTTCCGGGAATGCTCTGGCAAAAGTGTGGCCCATCATTCGAATGAA 1143
Qy 126 ---TyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuCysArg 144
Db 1144 CCGTAGCAACCGAAGCC-----ATTCTCCAGCCACCTTGAACCTGATGGCG 1191
Qy 145 ProValLeuSerProMetAsnLeuSerLeuHisThrAlaSerGlyLeuArgSerPhe 164
Db 1192 GGCANAAGTACACCCATGATGTGCTCAGAGTGGAGTGGCGGACGCGGACACAGCATT 1251
Qy 165 -----SerValLeuSerLeuAlaTyrGlyPheLeuAlaAspValAspLeuGluSer 181

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b 1252 GTGATGTACTCTCTCGTGGTGGGCTGGGCTGATAGCGGACATCGATATAGAGAGC 1311
Y 182 AsplysTyArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAla 201
b 1312 GAGCGATTGAGATCGATTGGAGCGCAAAAGTTTACGTTGTGGCCATCAAGCGATTGATC 1371
Y 202 AlalaArgThrTyArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPheLys 221
b 1372 GGGCTGGCAGCTACAAAGCGCGAGTGCCTATCTA---CTGGGCAAG---GGCAAGAAG 1425
Y 222 ThrProAlaSerProVal----- 227
b 1426 GAACCA-----CCAGTGAAGCGGCTCGAGAGTTGCTCGAGAATCAACGGCTGCAGGA 1479
Y 228 ValValGlnGlnGlyProValAspAla-----HisLeuValProLeuGluGlu--- 243
b 1480 ATCGCTCATCTCTGCTCTGAATGCCGGGAATTCATGATCTACCCGAGGAGGAG 1539
Y 243 ----- 243
b 1540 GGGAGGCGGTCTTGGATGGAGAACAGTTGCCCGATGCCATATCTTTGGATCGTTCGGTT 1599
Y 243 ----- 243
b 1600 TACGCCAGCATGCCAGATGTGCCTGCGCCATGTCCAGGCAACGGCATATTACTCC 1659
Y 243 ----- 243
b 1660 CTGGGCGGACCATGATCGATCCAAATCGACCGGATGACATTAGCCAGCGGATCGAG 1719
Y 244 -----GlnVal 245
b 1720 GCAGCAAAATCGGAATTCGCTGAGAGGCGTCCAAAGCGGACCATTCACCATACAGATG 1779
Y 246 Pro-----SerHisTrpGlnValValProAspGluAspPheValLeuValLeuAla 262
b 1780 CCATGCTCAGCAGCATGTTGGATCTGGAGATGTCGAGATGTCATTTGGATGGTCCATGCC 1839
Y 263 LeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCysAlaAla 282
b 1840 GCCTATACCAACCATCTCTCTCGATGTCCTTTTCGGCCCGAATCCCGTCTCGACGAT 1899
Y 283 GlyValMetHisLeuPheTyValArgAlaGlyValSerArgAlaMetLeuLeuArgLeu 302
b 1900 GGCCTCACTACCTGGTGATCCGAGAGGCGTTAGTCGCCATCAGCTGCTCAATTTTC 1959
Y 303 PheLeuAlaMetGluLysGlyArgHisMetGluTyr---GluCysProTyrLeuValTyr 321
b 1960 ATGCTGAACCTAAAGCAGGACCCCATCTGCCCATCGCGAGGATCGTTTCATCAAGGTG 2019
Y 322 ValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaValAsp 341
b 2020 GTGCTTGTGGGCATTCGGCATCGAGCGGACGAGCTCCGATGGCATCTGTGGTGGAC 2079
Y 342 GlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisPro 356
b 2080 GCGAGCGGGTGAATATGACCATTCAGCGGAGGTATGCCC 2124
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RESULT 15

S-10-348-052-25

Sequence 25, Application US/10348052

Publication No. US20030219782A1

GENERAL INFORMATION:

APPLICANT: Saba, Julie D.

TITLE OF INVENTION: Fyrtst, Henrik

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION

OF SPHINGOLIPID METABOLISM AND/OR SIGNALING

FILE REFERENCE: 200116, 405

CURRENT APPLICATION NUMBER: US/10/348,052

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 25

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; LENGTH: 2609
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-348-052-25
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Alignment Scores:

| Pred. No.: | 1-16e-50 | Length: | 2609 |
|------------------------|----------|---------------|------|
| Score: | 492.90 | Matches: | 139 |
| Percent Similarity: | 45.15% | Conservative: | 61 |
| Best Local Similarity: | 31.38% | Mismatches: | 131 |
| Query Match: | 24.44% | Indels: | 113 |
| DB: | 15 | Gaps: | 11 |

US-09-784-810C-2 (1-384) x US-10-348-052-25 (1-2609)

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QY 16 ArgValLeuValLeuLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArg 35
Db 755 CGAGTGCTTGTCTGTGAATCCAAATCCGGTCCGGTGAAGCTCGTGAAGTCTTCAAC 814
QY 36 SerHisValGlnProLeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGlu 55
Db 815 ATGCAGTGAACCCCGTGTCTCAACGAGCGGAGGTGCCCTAGCAGCTGTATGTATACCAAG 874
QY 56 ArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeu 75
Db 875 CATTCCAACTTTTGCATCGAGTTCTTGAGCACCAAGTGCCTGGACGCTGTGTGTCGGTG 934
QY 76 ValValMetSerGlyAspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgPro 95
Db 935 GTGGGTGTGGCGGAGAGCGTCTCTCCACGAGATAGTCAATGGACTGCTGCAGCGCCAG 994
QY 96 AspTrpGluThrAlaIle---GlnIysProLeuCysSerLeuProAlaGlySerGlyAsn 114
Db 995 GACTGGGCCCATCGTCTGCTCATCTGGCACTGGGAATCATCTCTTGGCGCTCCGGAAT 1054
QY 115 AlaLeuAlaAlaSerLeuAsnHisTyArgGlyTyrGluGlnValThrAsnGluAspLeu 134
Db 1055 GGAATTTGGCGGCTCCATTTGCCAT-----TGTTACAACAAGCAGCATG 1096
QY 135 LeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerProMetAsnLeuLeuSer 154
Db 1097 CTA---GGAGTGTCTTACCGTAAATCAGTGGACGCGATTCACCATGGAGTGGTGGCGG 1153
QY 155 LeuHisThrAlaSerGlyLeuArgSer---PheSerValLeuSerLeuAlaTrpGlyPhe 173
Db 1154 GTGCAGCTGCAGAGT-----CGCTCCCTCTACTCTCTCTCTCATCGCTGGGCTGTG 1207
QY 174 IleAlaAspValAspValLeuGluSerAspLysTyArgArgLeuGlyGluMetArgPheThr 193
Db 1208 ATCTCGAGCGTGGACATCGAGAGCGGCGCATTCGCATGTTGGGCTACCGCGCTTACC 1267
QY 194 LeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyArgGlyArgLeuAlaThrLeu 213
Db 1268 GTGTGGACCCCTACCGTCTGTGTGAATCTGCGCACCTTACAACGCGCGAATCAGTATCTT 1327
QY 213 ----- 213
Db 1328 CTGACGCGACCATGAGGTGTCTCTCAACCCATACCGGTATGTGTCCCGCGGAGA 1387
QY 214 -----ProVal 215
Db 1388 ATGCAGAGCGCGGTAGTGCACACGCAATCGACATGTGAATGGCGCGCGCCCATC 1447
QY 216 GlyArgValGlyPheLeuThrProAlaSerProValValGlnGlnGlnGlnGlnGlnGln 235
Db 1448 TATCATTCAGTGTC---CGAGTACCTGCCACAGAGTTTTCGCGACGCTGATCTCCCTGGAGAC 1506
QY 236 AlaHis-----LeuValProLeuGlu----- 242
Db 1507 GTCCATCAATCAGTGTCTCCGCTCGAGGTGCGACAGCTGGTGTGTGGGGGAGATCGCGCG 1566
QY 243 -----GluGlnValPro----- 246
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Db 1567 CAGCTTTTACTATTTCATATCGGAGAGCATCTACCACAGTCTGGCGGATGAGAGCGAGTT 1626
Qy 246 ----- 246
Db 1627 CGCGGGCTGGCGGCGCCCTCGCTGGAACACCGGACAGCAGAACTACGCTCCGGCAAGCGA 1686
Qy 247 -----Ser-HisTyrGlnValValProAspG1 255
Db 1687 GCTGCCGATCTGAACGAACCGCTGTCGGAGGATCAGGGTTGG---CTGGTGAGGAGGG 1743
Qy 255 uAspPheValLeuValLeuAlaLeuHisSerHisLeuAlaSerGluMetPheAlaAl 275
Db 1744 CGAGTTTCGTATGATGCACGCCCTTTACACAGACCCATCTGGGCATCGACTGTCATTTTC 1803
Qy 275 aProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSe 295
Db 1804 GCCCAAGGCCACGCTGAACGACGCGACCATCTACCTGATCCTCATACGCGCGGCATCAG 1863
Qy 295 rArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMet---GluTyr 314
Db 1864 CGCGCGCACCTGCTGAGCTTCCTTACAAATGAGCTCCGGCACTCACCTGCCGAGTC 1923
Qy 314 rGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLysAspG1 334
Db 1924 GCACGACGACCATGTGAAGGTGCTGCGAGTGCAGTGCAGCATTCGCGCTGGAGCCCTACGCAA 1983
Qy 334 YLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGlyGlnVa 354
Db 1984 TCACGGCATCATCACGGTCGACGCGGAGCGGCTCGAGTTCCGGGCCCTCCAAAGCTGAGT 2043
Qy 354 LHisPro 356
Db 2044 CCGCGCG 2050
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Job time : 423 secs